

Qy	64	GCCGACATCGAGGTGCCAAACCTTTTCGGTCAATATGAGCTCTCGGAAAAGATTAGCCTGT	123
Db	65	ATCGACATCGAGGTGCCAAACCTTTCCGCTCGATGTGAACCTTTGGGGAAGATCAGCCTGT	124
Qy	124	TATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCGGAT	183
Db	125	TAT--CCTAGAGTAACTTTTATCCGTTGAGCGAGCGGCCT--TCACGCGGACCGTCGGAT	182
Qy	184	CATTAAAGCCGACATTAATCTCTGTTTAAATTTCTAAATTTTACAGTTAAATATATATTTA	243
Db	183	CACTAAGACCGGCTTTCGCCCTTGTTCGACTCTAGTCTTCAGTCAGCTCCCTTATA	242
Qy	244	TCCTTTATATAATAATAT-----AACATGTGCACCTCCGTTTT	282
Db	243	CCCTTTACACTCTTGGATGATTTCCATCCATCTGAGGGAACCTTTGTGCGCCTCAGTTAC	302
Qy	283	TATATAGGAGGAGACCGCCCGCAGTCAAACTATCTTATAATATTGTTAAAAATTTTGTTA	342
Db	303	CTTTTATGAGGCGACCGCCGAGTCAAACTGCCCCCTGAAACTGTCAANGTCCCTGATTC	362
Qy	343	TAAAAATTTTATAAGAAATTTATATATATATAAAATGGTATTTTCATTAAACAATTACATTA	402
Db	363	AGGATCGCCATTAGAAATCTACGCTCTCCAGAGTGGTCTCTCACTGATGGCTCAATTT	422
Qy	403	TTCCAAAAAATAATATTACTACTTCCCAATTAATCTATGTTATATATATATATTTTCAA	462
Db	423	CTCGGAAAGAAACTTTTCAACGCTCCCACTAGACTGGCAAGAAAGCCCAACCCAA	482
Qy	463	TATCTATTATAGTAAAGCTTCATAGGTCTTCTGCTCTTAATATATAAAGAAATCTGCATCT	522
Db	483	TTTCAAGATACAGTCAAGCTTCATAGGGCTTTTCTGTCGAAGTATGATTAATTCGCATCT	542
Qy	523	TCACAGATAATTTTATTTTCATTTAAGATTTTTTTTAAAGACAGCATTTTAAAGTCGTTACATCT	582
Db	543	TCAGAAATATGTCTATTTACCGAGTCTCTCTCCGAGACAGCGCCAGATCGTTAGCCT	602
Qy	583	TTCATCGAGGTC	594
Db	603	TTGTCGCGAGTC	614

RESULT 2	
BE230849/c	
LOCUS	BE230849 571 bp linear EST 07-JUL-2000
DEFINITION	SNOWAMCAQ05G06SK Onchocerca volvulus adult male cDNA (SAW98MLW-OVAM)
ACCESSION	BE230849
VERSION	BE230849.1
KEYWORDS	GI:8967072
SOURCE	EST.
ORGANISM	Onchocerca volvulus. Onchocerca volvulus Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE	1 (bases 1 to 571)
AUTHORS	Lizotte-Waniewski,M. and Williams,S.A.
TITLE	Genes expressed in adult male stage of Onchocerca volvulus
JOURNAL	Unpublished (1998)
COMMENT	Contact: Steven A. Williams

Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genomewsmith.edu
Seq primer: [valuescript sk](#).
Location/Qualifiers
1. 571
/organism="Onchocerca volvulus"
/db_xref="taxon:6282"
/clone="SW0vAMCAQ05G06"
/clone_lib="Onchocerca volvulus adult male cDNA
(SAW98MLW-OvAM)"

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/sex="male"
/dev_stage="adult"
/lab_host="XL1-Blue MRF"
/notes="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Six adult
male worms of Onchocerca volvulus were isolated from
consenting patients and quick frozen. Adult male mRNA was
converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 2 x 10E5 independent recombinants
and the average insert size is ~1100bp. The library was
constructed by Michelle Lizotte-Waniewski with worms
provided by Dr. Sara Lustigman. The library is available
from Dr. Steven A. Williams, email: genome@smith.edu."

BASE COUNT      148 a      109 c      162 g      152 t
ORIGIN

      Query Match      28.9%; Score 171.4; DB 9; Length 571;
      Best Local Similarity 62.0%; Pred. No. 2.8e-16;
      Matches 31; Conservative 0; Mismatches 171; Indels 23; Gaps 2;

Qy 1 GTATCGCTTTAATAGCGCAACAGACTTACCTTAAAAACATACTACTGCCTTAGGATCGCA 60
Db 510 GTATCACTTTAATCGGGAACAGCGCAACCTTGGGACCTTCTTCAGCCCGAGGATGTGA 451

Qy 61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGACACTCTCGAAAGATTAGCC 120
Db 450 TGAGTCGACATCGAGGTGCCAAACGGTGTGCTGATATGAACCTCTTGAACACCATCAGCC 391

Qy 121 TGTATCCCTAGATGAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 180
Db 390 TGTATCCCGGCGTACCTTTTATCCGTTGAGCGATGACCCT-TCCATACAGAATCACCG 332

Qy 181 GATCATTAAGACCCGACATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATATATAT 240
Db 331 GATCACTATGACCGACATTCGTCTCTCTGTTGTCAGCCCTGCGAGTCAGCGCAAGCTT 272

Qy 241 TTATCTTTTATATAATAA-----TATAACATTTGACACCTCCG 278
Db 271 GTGCCATTATACTATTAACTGTTTCGACCACTCTAGCTTACCTTCGACGCTCCG 212

Qy 279 TTTTATTAGGAGGACCGCCGCACTATCTTATAAATATGTTTAAAAATTTT 338
Db 211 TTACCTTTTAGGAGGCGACGCGCCGCACTCAACCTACCCACCACATATGCTCTAGTTCCA 152

Qy 339 GTTATAAAATTTTATAGAAATTTATATATATAATAAATGATTTTCATTAAACAATTACA 398
Db 151 GATAATGAACATAGTTAGATATCAAAAGTGTAAGGGTGGTATCTCAAGGTGCAGTCCA 92

Qy 399 TTATTTCACAAAAAATAATATTACTACTTCCCAATTTATCTTGTATATATATATATTT 458
Db 91 TTACAGCTAGCGCATAACTTCAAAGCCTCCCACTATCTCGCACATTACATTTTTTAATA 32

Qy 459 TCAATATCTATTANTAGTAAGCTTCAAGG 489
Db 31 GCAATATAAAGCTATAGTAAAGGTGCACGGG 1

RESULT 3
LOCUS      AI151682/c
DEFINITION      SMOVAFCAP07B11SK Onchocerca volvulus adult female cDNA
                (SAW98MLW-OVAF) Onchocerca volvulus cDNA clone SMOVAFCAP07B11 5',
                mRNA sequence.
ACCESSION      AI151682
VERSION        AI151682.1
KEYWORDS       GI:3680151
SOURCE         EST.
ORGANISM       Onchocerca volvulus.
                Onchocerca volvulus
                Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                Onchocercidae; Onchocerca.
REFERENCE      1 (bases 1 to 598)
AUTHORS       Lizotte-Waniewski, M. and Williams, S.A.

```

TITLE Genes expressed in adult female stage of *Onchocerca volvulus*
JOURNAL Unpublished (1998)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1..598
/organism="Onchocerca volvulus"
/db_xref="taxon:6282"
/clone="SWOVAFCP07B11"
/clone_lib="Onchocerca volvulus adult female cDNA
(SAW98MLW-OvAF)"
/sex="female"
/dev_stage="adult"
/lab_host="Xil-Blue MRF"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
xho I; Filarial nematode parasite of humans. Two adult
female worms of *Onchocerca volvulus* were isolated from
consenting patients and quick frozen. Adult female mRNA
was converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 7 x 10⁵ independent recombinants
and the average insert size is ~1100bp. The library was
constructed by Michelle Lizotte-Waniewski with worms
provided by Dr. Sara Lustigman. The library is available
from Dr. Steven A. Williams, email: genome@smith.edu."
BASE COUNT 154 a 124 c 166 g 151 t 3 others
ORIGIN
Query Match 28.9%; Score 171.4; DB 9; Length 598;
Best Local Similarity 60.9%; Pred. No. 2.8e-16;
Matches 357; Conservative 0; Mismatches 204; Indels 25; Gaps 4
QY 1 GTATCGCTTTAATAGGCGCAACGACTTACCCTTAAACATACATACTGCTTAGGATGCGA 60
DB 588 GTATCACTTTAATCGGNGANCAGNCAACCTT-GGACCTCTTCAGCCCGCAGGATGTGA 530
QY 61 TAAGCGGACATCGAGGTGCCAAACCTTT-TGCTCAATATGGACTCTCGGAAAGATTAGC 119
DB 529 TGAGTCGACATCGAGGTGCCAAAGGGGTGCTGCGATATGAACCTTTGAACACCATCAGC 470
QY 120 CTGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAAATTTATTAATAAATATATC 179
DB 469 CTGTTATCCCGCGGTACCTTTTATCCGTTAGCGATGACCGT-TCCATACAGATCAACC 411
QY 180 GGATCATTAAACCGCACATTAATCTCTTTAAATTTGTAATTTTACAGTTAATATATATA 239
DB 410 GGATCATTAGACCGACATTTGCTCTCTGCTTGGCTTGACGCTCGCAGTCAGGCAAGCT 351
QY 240 TTTATCTTTTATATAATAA-----TATAACATTTGTACACCTCC 277
DB 350 TGTGCCATTATACATTAAGCTGATTTCCGACCACTCTAGCTTACCTTCGACGCGCTCC 291
QY 278 GTTTTATATAGGAGGAGACCGCCGACGTCAAACTATCTTAATAATATGTTAAAAAATTT 337
DB 290 GTTACCTTTTATAGGAGGAGACCGCCGACGTCAAACTACCCAGCATACAATGTCTAGTTCC 231
QY 338 TGTTTATAAAATTTTATAAGAAATTTATATATATATAAAATGGTATTTTCAATTAACAATTAC 397
DB 230 AGATATGAACACATAGTTAGATATACAAAGGTGAAGGGGTGATCTCAAGGTCGACCTCC 171
QY 398 ATTATTTTCCAAAAAATAATATTACTACTTCCCAATTTTATCTGTTATATATATATATATT 457
DB 170 ATTACAGCTAGCGCCATAACTTCAAGGCTCCCACTATCTGCAATACATTTTATAT 111
QY 458 TTCAATATCTATTAATAGTAAAGCTTCATAGGGTCTTTCTCTGCTTAAATATAAGAAATCTG 517

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QY 559 GACAGCATTTAAAGTCGTTACATCTTTTCATCGAGGTC 594
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Db 454 GACAGCATTTAAAGTCGTTACATCTTTTCATCGAGGTC 419

RESULT 5
BH504408/c 666 bp DNA linear GSS 13-DEC-2001
LOCUS BOHF234TR BOHF Brassica oleracea genomic clone BOHF234, DNA
DEFINITION sequence.
ACCESSION BH504408
VERSION BH504408.1 GI:17712505
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 666)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOHF234TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
Source 1..666
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHF234"
/clone_lib="BOHF"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 152 a 165 c 213 g 136 t
ORIGIN
Query Match 28.5%; Score 169; DB 12; Length 666;
Best Local Similarity 58.6%; Pred. No. 6.1e-16;
Matches 363; Conservative 0; Mismatches 230; Indels 26; Gaps 3;

QY 1 GTATCGCTTTAATAGCGGAACAGACTTACCCCTTAAACATACTACTGCGCTTAGGATGCGA 60
Db 642 GTACCGCTTTAATAGCGGAACAGCGCAACCCCTTGAACATACTACTACAGCCCGAGTGGCGA 583

QY 61 TAAGCCGACATCGAGGTGCGCAACCCCTTTCGTCGAATATGACCTCGGAAAGATTAGCC 120
|||||
Db 582 AGAGCCGACATCGAGGTGCGCAACCCCTTCCGCTCGATGTGAGCTCTTGGGGAAGATCAGCC 523

QY 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGGATAATTTTATTAATAATTAATATCG 180
|||||
Db 522 TGTATCCCTAGAGTAACCTTTTATCCGTTGAGCGACGCGCCCTCCACT-CGGCACCGTCG 464

QY 181 GATCATTAAAGACCGACATTAATCTCTGTTTAAATTTGTAATTTTACAGATTAATATATAT 240
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Db 463 GATCATTAAAGCGGACCTTTCGTCGCCCTGCTCGACGGGTGGGTCTTTCGACTCAAGCTCCCTT 404

QY 241 TTATCTTTATATATA-----AATATAACATTTGTACACCTCCG 278
|||||
Db 403 CTGCTTTTGCACCTCGAGGGGCAATCTCCGTCGCGCCCGAGGAAACCTTTGACGCGCTCCG 344

QY 279 TTTTATATAGAGGAGACCGCCCACTCAAACTATCTTATAAATATTGT---TAAAAAT 335
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Db 343 TTACCTTTTGGAGGCTACGCCCCATAGAACTGTCTACCTGAGACTGTCCCTTGGCCC 284

QY 336 TTTGTTATAAAAAATTTTATAAGAAATTTATATATATATAATAAATGGTATTTCATTAACAATT 395
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Db 283 GTAGGTCCTGCACACAAGGTTAGAATTCTAGCTCTTCCAGAGTGGTATCTCACTGATGGCT 224
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QY 396 ACATTATTTCCAAAAAATAATATTACTACTTCCATTTTATCTCTATCTATATATATATA 455
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Db 223 CGGGCCCCCGGAAGGAGGCGCTTCTTCGCCCTTCCACCTAAGCTGCGCAGGAAAGCCCA 164
|||||
QY 456 TTTTCAATATCTATTAACTAGTAAGCTTTCATAGGCTTTCCTGTCCTTAATAATAAGAAATC 515
|||||
Db 163 AAGCCAATCCAGGACAGTGAAGCTTTCATAGGCTTTCCTGTCAGGTCGAGGTAGTC 104
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QY 516 TGCATCTTCCACAGATAATTTTATTTTATTCAATTAAGATTTTTTTTAAGACAGCATTTAAGTCGT 575
|||||
Db 103 CGCATCTTCCACAGACATGTCTATTTCACCGAGCGCTCTCTCCGAGACAGTGCACGATCGT 44
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QY 576 TACATCTTTCATCGAGGTC 594
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Db 43 TAGCGCTTTTCGTGCGGGTC 25

RESULT 6
BH466711/c 671 bp DNA linear GSS 13-DEC-2001
LOCUS BOGRN92TR BOGR Brassica oleracea genomic clone BOGRN92, DNA
DEFINITION sequence.
ACCESSION BH466711
VERSION BH466711.1 GI:17667845
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 671)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGRN92TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
Source 1..671
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGRN92"
/clone_lib="BOGR"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 152 a 165 c 214 g 140 t
ORIGIN
Query Match 28.5%; Score 169; DB 12; Length 671;
Best Local Similarity 58.6%; Pred. No. 6.1e-16;
Matches 363; Conservative 0; Mismatches 230; Indels 26; Gaps 3;

QY 1 GTATCGCTTTAATAGCGGAACAGACTTACCCCTTAAACATACTACTGCGCTTAGGATGCGA 60
Db 655 GTACCGCTTTAATAGCGGAACAGCGCAACCCCTTGAACATACTACTACAGCCCGAGTGGCGA 596

QY 61 TAAGCCGACATCGAGGTGCGCAACCCCTTTCGTCGAATATGAGCTCTCGGAAAGATTAGCC 120
|||||
Db 595 AGAGCCGACATCGAGGTGCGCAACCCCTTCCGCTCGATGTGAGCTCTTGGGGAAGATCAGCC 536

QY 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGGATAATTTTATTAATAATTAATATCG 180
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Db 535 TGTTATCCCTAGAGTAACTTTTATCCGTTGAGCGACGGCCCTTCCACT-CGGCACCGCTCG 477
QY 181 GATCATTAAAGACGACATTAATCTCTGTAAATTTGTAATTTTACAGTTAAATATATAT 240
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Db 476 GATCATAAGGCGAGCTTTCGTCCTCGTGCAGGGTGGTCTTTCAGTCAAGCTCCCTT 417
QY 241 TTATCTTTTATATATA-----ANATAAACAATTTGACACCTCCG 278
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Db 416 CTGCTTTTGCACTCGAGGGCCAATCTCCGTCGCGCCCGAGGAAACCTTTGCACGCTCCG 357
QY 279 TTTTATATAGGAGAGACCGCCCACTCAAACTATCTTATAATATTGT---TAAAAAT 335
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Db 356 TTACCTTTTGGAGGCTCAGCCCCATAGAACTGTCTACCTGAGACTGCCCTTGGCCC 297
QY 336 TTTGTTATAAAAATTTTATAAGAAATTTATATATATAATAAATGGTATTTTCAATTAACAAT 395
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Db 296 GTAGGTCCTGACACAGGTTAGAAATCTAGCTCTCCAGAGTGGTATCTCACTGATGGCT 237
QY 396 ACATTATTTCCAAAAATAATTAATCTACTTCCCAATTTATCTATGTTATATATATA 455
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Db 236 CGGGCCCCCGGAGAGGCGCTTCTTCGCTTCCACCTAAGCTGCGCAGGAAAGCCCA 177
QY 456 TTTTCAATATCTATTAATAGTAAAGCTTATAGGCTTCTTCTGCTCAATATAAAGAAATC 515
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Db 176 AAGCCAAATCCAGGGAACAGTGAAGCTTCATAGGGCTTTCTGTCAGGTGCAAGTAGTC 117
QY 516 TGCATCTTCACAGATAAATTTTATTAAGATTTTAAAGACAGCATTTTAAGTCGT 575
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Db 116 CGCATCTTCACAGACATGTCTATTTCACCGAGCCTCTCTCCGAGAGTGCACCATCGT 57
QY 576 TACATCTTCATGCAAGTC 594
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Db 56 TACGCTTTTCGTGCGGGTC 38

RESULT 7
BH425423
LOCUS BH425423 BOHE Brassica oleracea genomic clone BOHEL23, DNA
DEFINITION sequence.
ACCESSION BH425423.1 GI:17611151
VERSION BH425423
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL 1 (bases 1 to 674)
COMMENT Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BOHEL23TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 674
/organism="Brassica oleracea"
/strain="tol000DH3"
/db_xref="taxon:3712"
/clone="BOHEL23"
/clone_lib="BOHE"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 139 a 214 c 167 g 154 t
ORIGIN
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Best Local Similarity 58.6%; Pred. No. 6e-16;
Matches 363; Conservative 0; Mismatches 230; Indels 26; Gaps 3;

QY 1 GTATCGCTTTAATAGCGAACAGACTTACCTTTAAAAACATACTACTGCTTACGATGCGA 60
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Db 44 GTACCGCTTTAATGGCGAACAGCCCAACCTTTGGAACATACACAGCCAGGTGCGA 103
QY 61 TAGCCGACATCGAGGTGCCAAACCTTTTCGTCAAATATGAGACTCTCGGAAAGATTAAGCC 120
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Db 104 AGAGCGGACATCGAGGTGCCAAACCTTTCCGTCGATGTGAGCTCTTGGGAAGATCAGCC 163
QY 121 TGTATTCCTTAGAGTAACTTTTATCCGTTAAGCGATAAATTTATTTAATAATTAATTA 180
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Db 164 TGTATTCCTTAGAGTAACTTTTATCCGTTGAGCGACGGCCCTTCCACT-CGGACCGCTCG 222
QY 181 GATCATTAAAGACGACATTAATCTCTGTTTAAATTTGTAATTTTACAGTTAAATATATAT 240
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Db 223 GATCACTAAGCGGACTTTTCGTCGACGGGTGGTCTTTCAGTCAAGCTCCCTT 282
QY 241 TTATCTTTTATATAA-----AATNTAACATTTGTACACCTCCG 278
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Db 283 CTGCTTTTGCACTCGAGGGCCAATCTCCGTCGCGCCCGAGGAAACCTTTGCACGCTCCG 342
QY 279 TTTTATATAGGAGAGACCGCCCACTATCTTATAAATATTGT---TAAAAAT 335
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Db 343 TTACCTTTTGGGAGGCTACGCCCCATAGAACTGTCTACTGAGACTGTCCTTGGGCC 402
QY 336 TTTGTTATAAAAAATTTTATAAGAAATTTATATATATAAATGTTATTTCAATTAACAAT 395
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Db 403 GTAGGCTCTGACACAAAGTTAGAAATCTAGCTCTTCAGAGTGGTATCTCACTGATGGCT 462
QY 396 ACATTATTTCCAAAAATAATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 455
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Db 463 CGGGCCCCCGGAGAGGAGGCTTCTTCGCTTCCACTAAGCTGCGAGGAAAGCCCA 522
QY 456 TTTTCAATATCTAATTAAGTTCATAGGCTTCTAGGCTCTTCTGCTCAATATAAAGAAATC 515
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Db 523 AAGCCAAATCCAGGACAGTGAAGCTTCATAGGCTTCTTCTCCAGGTGCGAGGTAGTC 582
QY 516 TGCATCTTCACAGATAAATTTTATTAAGATTTTATTAAGATTTTATTAAGATTTTATTA 575
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 583 CGCATCTTCACAGACATGTCTATTTCACCGAGCCTCTCTCCGAGACAGTCCCGAGATCGT 642
QY 576 TACATCTTCATGCAAGTC 594
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Db 643 TAGCGCTTTTCGTGCGGGTC 661

RESULT 8
BH562802
LOCUS BH562802 BOGM Brassica oleracea genomic clone BOGMW42, DNA
DEFINITION sequence.
ACCESSION BH562802
VERSION BH562802.1 GI:17814642
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL 1 (bases 1 to 684)
COMMENT Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BOGMW42TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
```


Qy	576	TACATCTTTTCAGGTC	594
Db	64	TACGCTTTCGTGGGGTC	46
RESULT 10			
BH472129			
LOCUS	BH472129	696 bp	DNA linear GSS 13-DEC-2001
DEFINITION	BOGQT90TF BOGQ Brassica oleracea genomic clone BOGQT90, DNA sequence.		
ACCESSION	BH472129		
VERSION	BH472129		
KEYWORDS	GSS.		
SOURCE	BH472129.1 GI:17680240		
ORGANISM	Brassica oleracea.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.		
AUTHORS	1 (bases 1 to 696)		
TITLE	Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.		
JOURNAL	Whole genome shotgun sequencing of Brassica oleracea unpublished (2001)		
COMMENT	Other_GSSs: BOGQT90TR Contact: Chris Town		
FEATURES	TIGR		
source	9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF Class: sheared ends.		
	location/Qualifiers		
	1..696		
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	/strain="To1000DH3"		
	/db_xref="taxon:3712"		
	/clone="BOGQT90"		
	/clone_lib="BOGQ"		
	/note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"		
BASE COUNT	144 a 222 c 171 g 159 t		
ORIGIN			
Query Match	28.5%; Score 169;	DB 12;	Length 696;
Best Local Similarity	58.6%;	Pred. No. 6e-16;	
Matches	363;	Conservative 0;	Mismatches 230; Indels 26; Gaps 3;
Qy	1	GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAACATACATACTACCTGCCCTAGGATCGGA	60
Db	41	TT	111
Db	41	GTACCGCTTTAATGGGCGAACAGCCCAACCTTCGGAACATACATACTACAGCCCAGGTGGCGA	100
Qy	61	TAAGCCGCATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC	120
Db	101	AGAGCCGACATCGAGGTGCCAAACCTTCCTCGATGTGAGCTCTTGGGGAAGATCAGCC	160
Qy	121	TGTTATCCCTAGAGTAACCTTTATCCGTTAAGCATTAATTTTATTAATAATAATATATCG	180
Db	161	TGTTATCCCTAGAGTAACCTTTTATCCGTTGAGCGAGCGCCCTTCCACT-CGGCACCCGTCG	219
Qy	181	GATCATTAAGACCGACATTAATCTCTGTTTAAATTTTGAAAAATTTTACAGTTAATATATAT	240
Db	220	GATCACTAAGCCGACCTTCGTCCTCGTCAGCGGGTGGGTCTTGCACTCAAGCTCCCTT	279
Qy	241	TTATCTTTTATATAATA-----AATATAACATTTGTACACCTCCG	278
Db	280	CTGCTTTTGCACTCGAGGGCCAATCTCGTCCGCCCGCAGGAACCTTTGCACGCCCTCG	339
Qy	279	TTTTTATATAGGAGGACCGCCCCAGCTCAACTATCTTATAATAATTTGT---TAAAAAT	335
Db	340	TTACTCTTTGGAGGCCCTACGCCCATAGAAACGTCTACTCTGAGACTGTCCTTTGGCCC	399

Db 121 TGTATCCCTAGATAAATTTTATCCCTTGAGGACGCGCCCTCCACT-CGGACCGCTCG 179
Qy 181 GATCATTAAGACCCACATTAATCTCTCTTTAAATTTGTAATTTTACAGTTAATATATAT 240
Db 180 GATCATAAGGCCGACCTTCGTCCTCTGCTGACGGGTGGGTCTTGACAGTCAAGTCCCTT 239
Qy 241 TTATCTTTTATAATA-----AATATAACAATTTGTACACCTCCG 278
Db 240 CTGCTTTTGCACTCGAGGGCCAATCTCCGTCGCGCCGAGGAACCTTTGCACGCTCCG 239
Qy 279 TTTTATATAGAGGACCGCCGAGTCAATCTCTTTAATAATTTGT---TAAAAAT 335
Db 300 TTACCTTTTGGAGGCTACGCGCCCAAGAACTGTCTACCTGAGACTGTCCCTTGGGCC 359
Qy 336 TTTCTTATAAATTTTATAGAATTTATATATATATAAATGGTATTCATTAAACAT 395
Db 360 GTAGGCTCTGACAAAGGTAGAAATCTAGCTCTCCAGAGTGGTATCTCACTGATGGCT 419
Qy 396 ACATTATTTCCAAAAAATAATATTAATCTTCCCTTATCTATGTTATATATATATA 455
Db 420 CGGCCCCCGGAGGAGGCTTCTTCGCTTCCACTTAAGCTGCGCAGGAAGCCCA 479
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Db 480 AAGCAATCCAGGGAACAGTGAAGCTTCATAGGCTCTTCTGCTCCAGGTGCAGGTAGTC 539
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Db 540 GCGATCTTCACAGACATGTCTATTTTCCAGGCTCTCTCCGAGACAGTGCCTCCAGATCGT 599
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Db 600 TACGCTTTTCGTGCGGTC 618

RESULT 12
BH466757/c
LOCUS
DEFINITION BH466757 704 bp DNA linear GSS 13-DEC-2001
BOHB Brassica oleracea genomic clone BOHB08, DNA
sequence.
ACCESSION BH466757
VERSION BH466757.1 GI:17668010
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOHB08TF
Contact: Chris Town
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
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/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHB08"
/clone_lib="BOHB"
/note="vector: pHOS1; site:1; BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 161 a 175 c 220 g 148 t

ORIGIN
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Best Local Similarity 58.6%; Pred. No. 6e-16;
Matches 363; Conservative 0; Mismatches 230; Indels 26; Gaps 3;
Qy 1 GTATCGCTTTAATAGCGAAGACACTTTACCTTTAAAAACATACTACTGCTTGGATGCGA 60
Db 660 GTACCGCTTTAATGGCGAAGACCCCAACCTTGGAACTACTACAGCCCGAGGTGGCGA 601
Qy 61 TAAGCGACATCGAGGTGCGCAACCTTTTCGTCAATATGGAATCTCGGAAAGATTAGCC 120
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Qy 121 TGTATCCCTTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTTAAATAATATATCG 180
Db 540 TGTATCCCTTAGAGTAACTTTTATCCGTTGAGCGACCGCCCTTCCACT-CGGACCGTCG 482
Qy 181 GATCATTAAAGACGACATTAATCTCTGTTTAAATTTTACAGTTAATATATAT 240
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Qy 241 TTATCTTTTATAATA-----AATATAACAATTTGTACACCTCCG 278
Db 421 CTGCTTTTGCACTCGAGGGCCAATCTCCGTCGCGCCGAGGAACCTTTGCACGCTCCG 362
Qy 279 TTTTATATAGAGGACCGCCGAGTCAATCTTATATAATATTTGT---TAAAAAT 335
Db 361 TTACCTTTTGGAGGCTACGCGCCCAAGAACTGTCTACTGAGACTGCTCCCTTGGGCC 302
Qy 336 TTTGTTATAAATTTTATAAGAAATTTATATATATAAATGGTATTTCAATTAACAT 395
Db 301 GTAGGCTCTGACACAAGTTAGAAATCTAGCTCTTCCAGAGTGTCTACTGATGGCT 242
Qy 396 ACATTATTTCCAAAAAATAATATTAATCTTCCACTTCCACTTAAGCTGCGCAGGAAGCCCA 455
Db 241 CGGCCCCCGGAGGAGGCTTCTTCGCTTCCACTTAAGCTGCGCAGGAAGCCCA 182
Qy 456 TTTTCAATATCTAATAGTAAGCTTCATAGGCTCTTCTGCTCTTAATATAAGAAATC 515
Db 181 AAGCAATCCAGGGAACAGTGAAGCTTCATAGGCTCTTCTGCTCCAGGTGCAGGTAGTC 122
Qy 516 TGCATCTTCACAGATAATTTATTTCAATTAAGATTTTATTAAGACAGCATTTAAGTCGT 575
Db 121 CGCATCTTCACAGACATGTCTATTTTCCAGGCTCTCTCCGAGACAGTGCCTCCAGATCGT 62
Qy 576 TACATCTTTCATCGAGTGC 594
Db 61 TACGCTTTTCGTGCGGTC 43

RESULT 13
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LOCUS
DEFINITION BH571671 709 bp DNA linear GSS 14-DEC-2001
BOHQ222TF BOHQ Brassica oleracea genomic clone BOHQ222, DNA
sequence.
ACCESSION BH571671
VERSION BH571671.1 GI:17823510
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 709)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOHQ22TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523

Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES

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/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHQ222"
/clone_lib="BOHQ"

BASE COUNT 151 a 226 c 171 g 161 t
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

Query Match 28.5%; Score 169; DB 12; Length 709;
Best Local Similarity 58.6%; Pred. No. 6e-16;
Matches 363; Conservative 0; Mismatches 230; Indels 26; Gaps 3;

QY 1 GTATCGCTTTAATAGCGGACAGACTTACCCTTAAACATACACTACTGCTTAGGATGCGA 60
Db 63 GTACCCCTTTAATGGCGGACAGCGCAACCCCTTGGAAACATACACTAGAGCCCGGCGGA 122
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QY 181 GATCATTAAGACCGACATTAATCTCTGTTTAAATTTTCAATTTACAGTTAATATATAT 240
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QY 241 TTATCTTTTATATAATA-----AATATAACATTTGTACACCTCCG 278
Db 302 CTGCTTTTGCACCTCGAGGGCCAATCTCCGTCGGGCCCGAGGAAACCTTTGACGCGCTCCG 361
QY 279 TTTTATATAGAGGAGACGCGCCAGTCAAACTATCTTATAAATTTGT---TAAAAAT 335
Db 362 TTACCTTTTGGGAGGCGCTACGCGCCCATAGAAACTGTCTACCTGAGACTGTCCCTTGGGCC 421
QY 336 TTTGTTTATAAATAATTTATAAGAAATTTATATATATAAATGGTATTTTCAATTAACAAT 395
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QY 396 ACATTATTTCCAAAAAATAATTAATTAATTTTCCCAATTTTATCTATGTTATATATATA 455
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QY 516 TGCATCTTCACAGATAATTTTATTCATTAAGATTTTATTAAGCAGCATTTAAGTCGT 575
Db 602 CGCATCTTCACAGACATGTCTAATTTACCGAGCCTCTCTCCGAGACAGATGCCAGATCGT 661
QY 576 TACATCTTTCATGCGAGGTC 594
Db 662 TACGCTTTTCGTGCGGTC 680

RESULT 14
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LOCUS BH537063
DEFINITION BOGWR91TR BOGW Brassica oleracea genomic clone BOGWR91, DNA
sequence.
ACCESSION BH537063
VERSION BH537063.1 GI:17772627

KEYWORDS
SOURCE
ORGANISM

GSS.
Brassica oleracea.
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 721)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGWR91TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers

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/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOGWR91"
/clone_lib="BOGW"
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BASE COUNT 163 a 176 c 230 g 152 t
ORIGIN

Query Match 28.5%; Score 169; DB 12; Length 721;
Best Local Similarity 58.6%; Pred. No. 5.9e-16;
Matches 363; Conservative 0; Mismatches 230; Indels 26; Gaps 3;

QY 1 GTATCGCTTTAATAGCGGACAGACTTACCCTTAAACATACACTACTGCTTAGGATGCGA 60
Db 657 GTACCCCTTTAATGGGGAACAGCCCAACCCCTTGGAAACATACACTAGAGCCCGGCGGA 598
QY 61 TAAGCGGACATCGAGTGGCGCAACCCCTTTGCTCAATATGAGCTCTCGGAAAAGATTAGCC 120
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QY 181 GATCATTAAGACCGACATTAATCTCTGTTTAAATTTTGTAAATTTTACAGTTAATATATAT 240
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QY 241 TTATCTTTTATATAATA-----AATATAACATTTGTACACCTCCG 278
Db 418 CTGCTTTTGCACCTCGAGGGCCAATCTCCGTCGGGCCCGAGGAAACCTTTGACGCGCTCCG 359
QY 279 TTTTATATAGGAGGAGACGCGCCAGTCAAACTATCTCTATAAATTTGT---TAAAAAT 335
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QY 336 TTTGTTTATAAATAATTTATAAAGAAATTTATATATATAAATGGTATTTTCAATTAACAAT 395
Db 298 GTAGGTCTTGACACAAGGTTAGAAATTTCTAGCTCTTCCAGAGTGGTATCTCACTGATGGCT 239
QY 396 ACATTATTTCCAAAAAATAATTAATTAATTTTCTACTTCCCAATTTATCTATGTTATATATA 455
Db 238 CGGGCCCCCGGAGGAGGCGCTTCTTCCGCTTTCCACCTTAAGCTGGCGAGGAAAGCCCA 179
QY 456 TTTTCAATATCTAATTAATAGTAAGCTTCATAGGCTTCTTCTCTCTAATATAAAGAAATC 515
Db 178 AAGCCAAATCCAGGGAACAGTGAAGCTTCTATAGGGTCTTCTGTCAGGTGCGAGGTAGTC 119
QY 516 TGCATCTTCACAGATAATTTTATTTTATTAAGATTTTATTTTAAAGACAGCATTTAAGTCGT 575

Db	118	CGATCTTACAGACATGCTATTTACCGAGGCTCTCCGAGACAGTGCACAGATCGT	59
Qy	576	TACATCTTTCATGCGAGTTC	594
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Db	337	TTACCTTTTGGGAGGCGCTACGCCCATAGAAACTGTCTACCTGAGACTGFCCTTGGCCC	278
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Db	277	GTAGGTCTTGACACAGAGTTTGAATCTAGCTCTCCAGAGTGGTATCTCACTGATGGCT	218
Qy	396	ACATTATTTCCAAAAAATAATATTACTACTTCCCATTATTTCTATGTATATATATATA	455
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Qy	456	TTTTTCAATCTATTATATAGTAAGACTTCATAGGGTCTTCTCTCTCTAATATAGAANAAT	515
Db	157	AAGCCAATCCAGGGAACAGTGAAGCTTCATAGGGTCTTCTCTCCAGGTGCAAGGTAGTC	98
Qy	516	TGCATCTTCACAGATATATTTATTTTCATTAAGATTTTTTTTAGACAGCATTTTAAGTCGT	575
Db	97	CGCATCTTCACAGACATGTCTATTTTACCAGGCGCTCTCTCCGAGACAGTGCCCGATCGT	38
Qy	576	TACATCTTTTCATGCAGCT	594
Db	37	TACGCTTTTCGTGGGCT	19

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Job time : 1716 secs

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OM nucleic - nucleic search, using sw model

Run on: October 17, 2002, 10:09:38 ; Search time 48 Seconds
(without alignments)
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Perfect score: 594
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Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	170	28.6	1869	US-08-371-377-21	Sequence 21, Appl
C 2	166	27.9	2904	US-09-463-355-3	Sequence 3, Appl
C 3	154.2	26.0	411529	US-09-103-840A-1	Sequence 1, Appl
C 4	142	23.9	2542	US-09-187-946-3	Sequence 3, Appl
C 5	72.8	12.3	433	US-08-875-972-25	Sequence 25, Appl
C 6	72.8	12.3	16569	US-09-097-889-2	Sequence 2, Appl
C 7	72.8	12.3	16569	US-09-377-856-1	Sequence 1, Appl
C 8	66.4	11.2	639	US-08-998-416-188	Sequence 188, App
C 9	65.8	11.1	19124	US-08-487-826B-13	Sequence 13, Appl
C 10	64.6	10.9	629	US-08-454-557C-43	Sequence 43, Appl
C 11	64.6	10.9	629	US-08-340-426D-43	Sequence 43, Appl
C 12	64.6	10.9	629	US-08-450-673C-43	Sequence 43, Appl
C 13	64.6	10.9	629	PCT-US95-17111A-43	Sequence 43, Appl
C 14	63.6	10.7	19124	US-08-487-826B-13	Sequence 13, Appl
C 15	59.2	10.0	665	US-08-883-795A-36	Sequence 36, Appl
C 16	58.4	9.8	3095	5231168-1	Patent No. 5231168
C 17	57.6	9.7	4256	US-08-505-509-31	Sequence 31, Appl
C 18	57.6	9.7	4256	US-08-491-690A-31	Sequence 31, Appl
C 19	57.4	9.7	2061	US-09-187-946-4	Sequence 4, Appl
C 20	57	9.6	6124	US-08-213-419B-3	Sequence 3, Appl
C 21	56.2	9.5	615	US-08-998-416-186	Sequence 186, App
C 22	56	9.4	688	US-08-998-416-972	Sequence 972, App
C 23	55.2	9.3	8920	US-08-446-855A-1	Sequence 1, Appl
C 24	55.2	9.3	8920	US-09-150-741-1	Sequence 1, Appl
C 25	54.6	9.2	1431	US-09-316-083-2	Sequence 2, Appl
C 26	54.6	9.2	6152	US-08-973-462-1	Sequence 1, Appl
C 27	54.4	9.2	429	US-08-991-789A-215	Sequence 215, App

C 28	54.4	9.2	429	4	US-09-062-451-215	Sequence 215, App
C 29	54.4	9.2	675	4	US-08-998-416-179	Sequence 179, App
C 30	54.4	9.2	676	4	US-08-998-416-280	Sequence 280, App
C 31	54.4	9.2	685	4	US-08-998-416-951	Sequence 951, App
C 32	54.4	9.2	2058	2	US-08-749-391-1	Sequence 1, Appl
C 33	54.4	9.2	2058	3	US-09-390-200-1	Sequence 1, Appl
C 34	54.2	9.1	665	2	US-08-883-795A-36	Sequence 36, Appl
C 35	54	9.1	837	4	US-08-998-416-288	Sequence 288, App
C 36	53.8	9.1	6243	2	US-09-056-075-1	Sequence 1, Appl
C 37	53.6	9.0	615	4	US-08-998-416-186	Sequence 186, App
C 38	52.8	8.9	636	4	US-08-998-416-1137	Sequence 1137, App
C 39	52.6	8.9	6768	1	US-08-107-755A-1	Sequence 1, Appl
C 40	52.6	8.9	8457	1	US-07-991-867B-1	Sequence 1, Appl
C 41	52.6	8.9	8457	2	US-08-544-332-1	Sequence 1, Appl
C 42	52.4	8.8	2564	1	US-08-224-983-1	Sequence 1, Appl
C 43	52.4	8.8	2564	2	US-08-852-933-1	Sequence 1, Appl
C 44	52.4	8.8	2564	2	US-08-852-945-1	Sequence 1, Appl
C 45	52.4	8.8	2564	2	US-08-853-021-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-371-377-21/c
; Sequence 21, Application US/08371377
; Patent No. 5851764

; GENERAL INFORMATION:

; APPLICANT: Fisher, Paul B.

; APPLICANT: Shen, Ruqian

; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND

; TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED
MOLECULES AND TRANSFORMATION-ASSOCIATED GENES

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/371,377

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/37590-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1869 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-371-377-21

Query Match 28.6%; Score 170; DB 2; Length 1869;

Best Local Similarity 60.9%; Pred. No. 1e-26; Indels 26; Gaps 5;
Matches 375; Conservative 0; Mismatches 215;

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QY 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATAAATTATCG 180
Db 1701 TGTATCCCGGGTGACTTTTATCCGTTGAGCGACGGCCAT-TCCACATGTACCGCG 1643
QY 181 GATCATTAAAGACCGACATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATATATAT 240
Db 1642 GATCATAAGTCTCTGCTTTCGCACTGCTGCACTTGTAAAGTCTTGCACTCAACCACTT 1583
QY 241 TTATCTTTAT-----ATAATAATAATAACATTTGTACACCTCCG 278
Db 1582 TTACTTTGTCTCTGCATATGTTCTGACCAATTTGAGTGTAGCTTTGAAGCGCTCCG 1523
QY 279 TTTTATATAGGAGGAGACCGCCCGCAGTCAAACTATCTTATAAATATTGTTAAAAATTTT 338
Db 1522 TTACACTTTAGGAGCGGACCG-CCCACTCAAACTACCCACCGCACTG-TCTCCTTCCA 1465
QY 339 GTTATAAAATTTTAAAGAAATTTATATATATAATAAATGGTATTTCAATTAACAATTACA 398
Db 1464 GATAAGGGAACGGGTTAGAAAATCAATTTAGCAAGGTTGTTTCAAGGTTGACTCCA 1405
QY 399 TTAATTTCAAAAAATAATATCTACTTCCCTATTTATCTATTTATCTATATATATATATTT 458
Db 1404 CTAGACTAGGCTCCAGCTTCAAAAGTCTCCCGCTATCTACACATGCTFAAACCAATTT 1345
QY 459 TCAATATCTATTAAATAGTAAGCTTTCATAGGGTCTTTCTGCTCAATATTAAGAAATCTGC 518
Db 1344 TCAATACGAAGTTTATAGTAAGCTCCACGGGCTCTTTCTGCTTGATGCGGGTAACTGC 1285
QY 519 ATCTTCACAGATAATTTTATTTCAATTAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTAC 578
Db 1284 GTTTTCACTGTACATAAATTTTCAACGAGTCCCAATGTTGAGACAGTAGGGAGATCATTCG 1225
QY 579 ATCTTTTCATGCAGGTC 594
Db 1224 GCCTTTCGTGCAGGTC 1209
RESULT 2
us-09-465-355-3/c
; Sequence 3, Application US/09465355
; Patent No. 6316194
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Knowles, David
; APPLICANT: Murchie, Alastair
; APPLICANT: Lentzen, Georg
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials
; FILE REFERENCE: 22620/1150 (Formerly 3950/85276)
; CURRENT APPLICATION NUMBER: US/09/465,355
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/325,601
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: GB 9812196.5
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9904790.4
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/122,439
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/088,241
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2904
; TYPE: RNA
; ORGANISM: Escherichia coli

US-09-465-355-3
Query Match 27.9%; Score 166; DB 4; Length 2904;
Best Local Similarity 57.3%; Pred. No. 7e-26;
Matches 353; Conservativity 0; Mismatches 240; Indels 23; Gaps 2;
QY 1 GTATCGCTTTAATAGCGGAACAGACTTTACCTTTAAAAACATACTACTGCTTCTAGGATGCGA 60
Db 2574 GTACCACTTTAATAGCGGAACAGCATACCTTTGGGGACCTACTTCAGCCCGGATGTGA 2515
QY 61 TAAGCCGACATCGAGGTGCCAAACCTTTTTCGTCAAATATGAGACTCTCGGAAAGATTAGCC 120
Db 2514 TGAGCCGACATCGAGGTGCCAAACACCGCGCTCGATATGAATCTTGGGCGGTATCAGCC 2455
QY 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATAAATTATCG 180
Db 2454 TGTATCCCGGGTAGTACCTTTTATCCGTTGAGCGATGGCCCTTCCCAT-T-CAGAACCACCG 2396
QY 181 GATCATTAAAGACCGACATTAATCTCTGTTTAAATTTTGTAAATTTTACAGTTAATATATAT 240
Db 2395 GATCACTATGACCTGCTTTCGCACTGCTCGCGCGTCAAGCTCAAGCTGGCTT 2336
QY 241 TTATCTTT-----ATAATAATAATAAATTTGTACACCTCGG 278
Db 2335 ATGCCATTGCACTTAACCTCTGATGCCGACGAGGATTAGCCACCTTCGCTCCTCCG 2276
QY 279 TTTTATATAGGAGGAGACCGCCCGCAGTCAAACTATCTTATAAATATTGTTAAAAATTTT 338
Db 2275 TTACTCTTTAGGAGGAGACCGCCCGCAGTCAAACTACCCACGACACTGTCCGCAACCGG 2216
QY 339 GTTATAAAATTTTATAAAGAAATTTATATATATATAATAAATGGTATTTTCATTAAACAATTACA 398
Db 2215 GATTACGGGTCAACGTTAGAACATCAAAACATTAAGGGTGGTATTTCGAAGGTCCGCTCCA 2156
QY 399 TTAATTTCCAAAAAATAATATTAATTAATCTTCCCATTTTATCTATGTTATATATATATTT 458
Db 2155 TGAGACTGGCGTCCACACTTCTAAGCCCTCCACCTATCTACACATCAAGGCTCAATGT 2096
QY 459 TCAATATCTATTAAATAGTAAGCTTTCATAGGGTCTTTCTGCTCAATATAAAGAAATCTGC 518
Db 2095 TCAGTGTCAAGCTATAGTAAGGTTTACGGGGTCTTTCCGCTTTCGCGCGGTACACTGC 2036
QY 519 ATCTTCACAGATAATTTTATTTTCAATTAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTAC 578
Db 2035 ATCTTCACAGCGAGTTCAATTTTCACTGAGTCTCGGGTGGAGACAGCGCTGGCCATCATAC 1976
QY 579 ATCTTTTCATGCAGGTC 594
Db 1975 GCATTCGTGCAGGTC 1960
RESULT 3
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

[illegible]

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1      RESULT 5
2      US-08-875-972-25/c
3      ; Sequence 25, Application US/08875972
4      ; Patent No. 5985564
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Huntington Potter and Jinhue Li
7      ; TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
8      ; TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
9      ; NUMBER OF SEQUENCES: 29
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
12     ; STREET: Two Millita Drive
13     ; CITY: Lexington
14     ; STATE: Massachusetts
15     ; COUNTRY: USA
16     ; ZIP: 02173-4799
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: Floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/875,972
24     ; FILING DATE: 08-AUG-97
25     ; CLASSIFICATION: 435

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; FILING DATE: 08-AUG-97
 ; CLASSIFICATION: 435
 ;

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,448
; FILING DATE: 16-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan Esq., Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-03PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-875-972-25

Query Match 12.3%; Score 72.8; DB 2; Length 433;
Best Local Similarity 62.8%; Pred. No. 5.1e-07;
Matches 113; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 1 GTATCGCTTTAATAGGCGAACAGACTTACCCCTTAAACATACACTGCTCGGAAAGATTAGCG 60
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 258 GTAGGACTTTAATCGTTGAACAAACGAACCTTTAATAGCGGCTGCACCATCGGGATGTC 199

Qy 61 TAAGCCACATCGAGGTCGCAACACCTTTTCGTCATATGACTCTCGGAAAGATTAGCG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 TGATCCACATCGAGGTCGTAACCCCTATTGTTGATGACTCTAGAATAGGATTGCGC 139

Qy 121 TGTATCCCTAGACTACTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 TGTATCCCTAGGTAACCTTGTCCGTTGTCAGTATTGGATCAATTCAGTATAGTAG 79

RESULT 6
US-09-097-889-2/c
; Sequence 2, Application US/09097889
; Patent No. 621817
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.417
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 16569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-097-889-2

Query Match 12.3%; Score 72.8; DB 4; Length 16569;
Best Local Similarity 62.8%; Pred. No. 7.3e-07;
Matches 113; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 1 GTATCGCTTTAATAGGCGAACAGACTTACCCCTTAAACATACACTGCTCGGAAAGATTAGCG 60
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3060 GTAGGACTTTAATCGTTGAACAAACGAACCTTTAATAGCGGCTGCACCATCGGGATGTC 3001

Qy 61 TAAGCCGACATCGAGGTCGCAACACCTTTTCGTCATATGACTCTCGGAAAGATTAGCG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3000 TGATCCACATCGAGGTCGTAACCCCTATTGTTGATGACTCTAGAATAGGATTGCGC 2941

Qy 121 TGTATCCCTAGACTACTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2940 TGTATCCCTAGGTAACCTTGTCCGTTGTCAGTATTGGATCAATTCAGTATAGTAG 2881

RESULT 7
US-09-377-856-1/c
; Sequence 1, Application US/09377856
; Patent No. 6344322
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; TITLE OF INVENTION: Markers
; FILE REFERENCE: 1107-82346
; CURRENT APPLICATION NUMBER: US/09/377,856
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-377-856-1

Query Match 12.3%; Score 72.8; DB 4; Length 16569;
Best Local Similarity 62.8%; Pred. No. 7.3e-07;
Matches 113; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 1 GTATCGCTTTAATAGGCGAACAGACTTACCCCTTAAACATACACTGCTCGGAAAGATTAGCG 60
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3060 GTAGGACTTTAATCGTTGAACAAACGAACCTTTAATAGCGGCTGCACCATCGGGATGTC 3001

Qy 61 TAAGCCGACATCGAGGTCGCAACACCTTTTCGTCATATGACTCTCGGAAAGATTAGCG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3000 TGATCCACATCGAGGTCGTAACCCCTATTGTTGATGACTCTAGAATAGGATTGCGC 2941

Qy 121 TGTATCCCTAGACTACTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2940 TGTATCCCTAGGTAACCTTGTCCGTTGTCAGTATTGGATCAATTCAGTATAGTAG 2881

RESULT 8
US-08-998-416-188
; Sequence 188, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippssen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 11.1%; Score 65.8; DB 2; Length 19124;
Best Local Similarity 51.6%; Pred. No. 2e-05;
Matches 181; Conservative 0; Mismatches 162; Indels 8; Gaps

Qy 137 ACTTTTATCGCTTAAGCGATAATTTTATTAATAAATTAATTCGGATCATTAAGACCGAC 196
Db 6773 ACTTTTATATGTTTCTGATTTTTCGTAATTTTTTTTCTCATTTTAATTTTACTTAATA 6832
Qy 197 ATTAATCTCTGTTTAATTTTGTAATTTTACAGTTAAATATATATATATCTTTTATATAA 256
Db 6833 AATAAACAATAAAAAAATAATATATATATAAATTAATAGATAAATAAGGAATACATAA 6892
Qy 257 AATATACATGTACACCTCGGTTTTTATATAGAGAGAGACGCCGCCGCAACTATCT 316
Db 6893 AATAATAATTTCTCGAATATATTTTTTTTTTGTAGAATATTTAAATTTATTATAAATTT 6952
Qy 317 TATAAATATGTTAAAAATTTTGTTATAAAAAATTTTATAAGAAAT-----TTATATAT 368
Db 6953 ATTAATATATATATATATTTTTTTTTTAAAAATATATAAACTAATAATTTATTATATAC 7012
Qy 369 ATATAAAATGATTTTCATTAAACAATTACATTAATTTCCAAAAAATAATTTACTACTTC 428
Db 7013 ATATAAATATATTTTTTAAACATACATATATTTGTAATATATAATAGTACAACTAT 7072
Qy 429 CCATTATTCATGTTATATATATATATATATTTTCAATATCTTAATAGTAAA 479
Db 7073 TAATATATATATATATATATACAATATTTTATATATTTGTAATACATAA 7123

RESULT 10
US-08-454-557C-43
; Sequence 43, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121

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```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 629 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
;
US-08-454-557C-43
;
Query Match 10.9%; Score 64.6; DB 2; Length 629;
Best Local Similarity 64.2%; Pred. No. 2.5e-05;
Matches 97; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

.Oy 18 GAACAGACTTACCCTTAAACATACTACTGCCTTAGGATCGGATAGCGGACATCGAGGT 77
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 206 GAACAAACGAACCTTTAATAGCGCTGCACCATCGGATGCTCTGATCCAAACATCGAGGT 265

Oy 78 GCCAAACCTTTTCGTCATATGACCTCGGAAACATAGCTGTATCCCTAGAGTAA 137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 266 CGTAAACCTTATGTTGATAGGACTCTAGATAGGATTCGCTGTATCCCTAGGTTAA 325

Oy 138 CTTTATCCGTTAAGCGATAATTTTATTATT 168
    ||| | | | | | | | | | | | | | | |
Db 326 CTTGTTCCGTTGGTCAAGTTATTGGATCAAT 356

RESULT 11
US-08-340-426D-43
; Sequence 43, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 14-NOV-1994
```

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;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 629 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
;
US-08-340-426D-43
;
Query Match 10.9%; Score 64.6; DB 2; Length 629;
Best Local Similarity 64.2%; Pred. No. 2.5e-05;
Matches 97; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Oy 18 GAACAGACTTACCCTTAAACATACTACTGCCTTAGGATCGGATAGCGGACATCGAGGT 77
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 206 GAACAAACGAACCTTTAATAGCGCTGCACCATCGGATGCTCTGATCCAAACATCGAGGT 265

Oy 78 GCCAAACCTTTTCGTCATATGACCTCGGAAACATAGCTGTATCCCTAGAGTAA 137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 266 CGTAAACCTTATGTTGATAGGACTCTAGATAGGATTCGCTGTATCCCTAGGTTAA 325

Oy 138 CTTTATCCGTTAAGCGATAATTTTATTATT 168
    ||| | | | | | | | | | | | | | | |
Db 326 CTTGTTCCGTTGGTCAAGTTATTGGATCAAT 356

RESULT 12
US-08-450-673C-43
; Sequence 43, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 629 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
;
US-08-450-673C-43
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Query Match          10.98;   Score 64.6;  DB 2;   Length 629;
Best Local Similarity 64.2%;   Pred. No. 2.5e-05;
Matches          97;  Conservative 0;  Mismatches 54;  Indels 0;  Gaps 0;

QY  18  GAACAGACTTACCCCTTAAACATACTACTCGCTTAGGATGCGATAAGCCGACATCGAGGT  77
      |||||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  206  GAACAACAGACCTTTAATACGGCTGCACCATCGGAGTGCTCGATCCACATCGAGGT  265
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY  78  GCCAAACCTTTTCGTCAATATGGACTCTCGGAAAGATATAGCCTGTTATCCCTAGAGTAA  137
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  266  CGTAAACCTATTGTTGATATAGGACTCTAGAATAGGATTGGCTCTTATCCCTAGGTTAA  325
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY  138  CTTTTTATCCGTTAAGCGATAATTTTATTATT  168
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  326  CTCTGTCGTTGGTCAAGTTATTGGATCAAT  356
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
PCT-US95-17111A-43
; Sequence 43, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609,3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 629 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
PCT-US95-17111A-43

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Qy 138 CTTTATCCGTTAAGCGATAAATTTTATTT 168
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Db 326 CTTGTCGTTGGTCAAGTTATTTGGATCAAT 356

RESULT 14
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Query Match 10.7%; Score 63.6; DB 2; Length 19124;
Best Local Similarity 52.5%; Pred. No. 5.5e-05;
Matches 166; Conservative 0; Mismatches 144; Indels 6; Gaps 1;

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Qy 218 AAATTTTACAGTTAAATATATATTTTATCTTTATATAAATAAATAACATGTGACACCTCC 277
Db 15713 TTTTTTTGGTTTATGATATATATTTTTTTTTTTTAAATGTTTTTTTTTCTCTTTT 15654

Qy 278 GTTTTATATAGGAGGAGCGCCCGCAACTACTCTTATAAATAATTTGTTAAATAATTT 337
Db 15653 GTTTTATTTTTTTTATAATC-----ATTTTTTTTATATAAATTTTTTTTAAATTT 15600

Qy 338 TGGTTAAAAAATTTTAAAGAATTTATATATATAATAAAATGGTATTTTCATTAACAATTC 397
Db 15599 TTTTGTGATATCTTTTTCATTTTATTTTATCTCAAAATTTATATTTTATTTATTAATATTTT 15540

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 17, 2002, 10:04:08 ; Search time 217 Seconds
(without alignments)
4699.757 Million cell updates/sec

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Perfect score: 594

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	100.0	5849	19	AAV331135 Plasmodium berghei
2	204	34.3	3398	20	AAV331135 Plasmodium berghei
3	204	34.3	116277	20	AAV331135 Plasmodium berghei
4	190	32.0	1385	22	AAV331135 Plasmodium berghei
5	190	32.0	2725	22	AAV331135 Plasmodium berghei
6	190	32.0	2869	22	AAV331135 Plasmodium berghei
7	190	32.0	3012	22	AAV331135 Plasmodium berghei
8	190	32.0	3012	22	AAV331135 Plasmodium berghei
9	190	32.0	3030	22	AAV331135 Plasmodium berghei

10	190	32.0	3086	22	AAH54819	S. epidermidis gen
11	190	32.0	3099	22	AAH54513	S. epidermidis gen
12	190	32.0	3229	22	AAH54504	S. epidermidis gen
13	190	32.0	3232	22	AAH54853	S. epidermidis gen
14	190	32.0	3405	22	AAH54539	S. epidermidis gen
15	190	32.0	3500	22	AAH54518	S. epidermidis gen
16	190	32.0	3513	22	AAH53987	S. epidermidis gen
17	190	32.0	3608	22	AAH54395	S. epidermidis gen
18	190	32.0	3625	22	AAH54294	S. epidermidis gen
19	190	32.0	3656	22	AAH54375	S. epidermidis gen
20	190	32.0	3716	22	AAH54078	S. epidermidis gen
21	190	32.0	3845	22	AAH54156	S. epidermidis gen
22	190	32.0	3929	22	AAH54246	S. epidermidis gen
23	190	32.0	3937	22	AAH54408	S. epidermidis gen
24	190	32.0	4106	22	AAH54320	S. epidermidis gen
25	188.4	31.7	892	23	AAH51075	Staphylococcus aur
26	188.4	31.7	2923	22	AAH89402	Staphylococcus aur
27	188.4	31.7	5048	21	AAH65735	Streptococcus pneu
28	188.4	31.7	5273	20	AAH24982	Haemophilus influe
29	188.4	31.7	5519	20	AAH24981	Haemophilus influe
30	188.4	31.7	6591	18	AAV77425	Staphylococcus aur
31	188.4	31.7	1830121	17	AAH242063	Haemophilus influe
32	185.2	31.2	269223	22	AAH28554	Genomic fragment #
33	178	30.0	2405	20	AAH13746	Enterococcus faeca
34	175.8	29.6	2922	20	AAH03532	Chlamydia trachoma
35	174	29.3	2904	21	AAH66047	E. coli proliferat
36	174	29.3	2904	21	AAH66052	E. coli proliferat
37	174	29.3	2904	22	AAH23016	E. coli 23S rRNA s
38	174	29.3	2904	22	AAH89403	Sequences from 23S
39	174	29.3	2907	19	AAH38096	Enterohaemorrhagic
40	174	29.3	2907	19	AAH38107	Enterohaemorrhagic
41	174	29.3	3118	22	AAH49806	Escherichia coli t
42	174	29.3	5097	20	AAH24983	E. coli MG1655 rrr
43	174	29.3	5105	20	AAH24989	E. coli MG1655 rrr
44	172.4	29.0	5090	20	AAH24988	E. coli MG1655 rrr
45	172.4	29.0	30246	18	AAV74367	Staphylococcus aur

ALIGNMENTS

RESULT 1
AAV33135
ID AAV33135 standard; DNA; 5849 BP.
XX
AC AAV331135;
XX
DT 07-DEC-1998 (first entry)
XX
DE Plasmodium berghei plastid PSI-PL470 gene.
XX
KW Malaria; infection; therapy; diagnosis; vaccine; plastid;
KW PSI-PL470 gene; ds.
XX
OS Plasmodium berghei ANKA strain.
XX
PN WO9835057-Al.
XX
PD 13-AUG-1998.
XX
PF 05-FEB-1998; 98WO-IB00212.
XX
PR 26-SEP-1997; 97AU-0009481.
PR 06-FEB-1997; 97AU-0004953.
PR 21-APR-1997; 97AU-0006329.
XX
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (UYSI-) UNIV SINGAPORE NAT.
XX
PI Kara AKU, Nelson JS, Tan TMC, Tham JM, Ting RCV;
XX WPI; 1998-447251/38.

PT Detecting Plasmodium infection from hybridisation with
PT extrachromosomal element - providing genus or species specific
PT diagnosis with few false negatives, in humans or animals
XX
PS Claim 15; Page 54-59; 120pp; English.

XX This is the nucleotide sequence of one strand of the PSI-PL470
CC gene of the 30.7 kb extrachromosomal plasmid of Plasmodium berghel.
CC This plasmid encodes organelle-like rRNAs, tRNAs, ribosomal
CC proteins and RNA polymerase subunits, amongst others. Plasmodium is
CC detected in a human or animal sample by treating it, or derived
CC nucleic acid, with a Plasmodium extrachromosomal genetic element or
CC derived nucleic acid (A) and detecting any hybridisation. (A) can
CC include the PSI-PL470, PLH-PPH, PRB or PWQ gene, the mitochondrial
CC coxI gene, and nucleic acids derived from them. Also new are
CC (A)-specific probes and primers (see AAV33139-56). The method is
CC used to diagnose Plasmodium infection. Also (not claimed) the
CC polypeptides encoded by (A) are useful as targets for drug
CC development and for development of anti-malaria vaccines. The high
CC degree of similarity between (A) from different species allows
CC development of genus- or species-specific assays that result in
CC fewer false negatives than known methods (typically 1% against 3%).
XX
SQ Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T; 0 other;

Query Match 100.0%; Score 594; DB 19; Length 5849;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAACATACACTACTCGCTTAGGATCGGA 60
Db 1147 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAACATACACTACTCGCTTAGGATCGGA 1206
QY 61 TAAGCGGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAGATTAGCC 120
Db 1207 TAAGCGGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAGATTAGCC 1266
QY 121 TGTATCCCTAGAGTAAGTATTTATCCGTTAAGCGGATAATTTTATTAATAATTAATATCG 180
Db 1267 TGTATCCCTAGAGTAAGTATTTATCCGTTAAGCGGATAATTTTATTAATAATTAATATCG 1326
QY 181 GATCATTAAGACCGACATTAATCTCTGTTAAATTTGTAATTTTACAGTTAATATATAT 240
Db 1327 GATCATTAAGACCGACATTAATCTCTGTTAAATTTGTAATTTTACAGTTAATATATAT 1386
QY 241 TTATCTTTATATAATAATAATAACATTTGTACACCTCGTCTTTTATATAGGAGGAGCCGC 300
Db 1387 TTATCTTTATATAATAATAATAACATTTGTACACCTCGTCTTTTATATAGGAGGAGCCGC 1446
QY 301 CCCAGTCAAACTATCTTATAAATATTTGTTAAAAATTTTGTATAAAAAATTTTATAAGAA 360
Db 1447 CCCAGTCAAACTATCTTATAAATATTTGTTAAAAATTTTGTATAAAAAATTTTATAAGAA 1506
QY 361 TTATATATATAATAAATGGATTTCATTAACAATACATATATTTCCAAAAAATAATATT 420
Db 1507 TTATATATATAATAAATGGATTTCATTAACAATACATATATTTCCAAAAAATAATATT 1566
QY 421 ACTACTCTCCCATTTATCTATGTTATATATATATATTTTCAATATCTATTAAATAGTAAAG 480
Db 1567 ACTACTCTCCCATTTATCTATGTTATATATATATATTTTCAATATCTATTAAATAGTAAAG 1626
QY 481 CTTTCATAGGGCTTTCTGTCCTAATAATAAGAAATCTGCATCTTTCACAGATAATTTTATTT 540
Db 1627 CTTTCATAGGGCTTTCTGTCCTAATAATAAGAAATCTGCATCTTTCACAGATAATTTTATTT 1686
QY 541 CATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTTCATCGAGGTC 594
Db 1687 CATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTTCATCGAGGTC 1740

RESULT 2

RAX20282/c

ID AAX20282 standard; DNA; 3398 BP.

XX
AC
XX
DT

04-MAY-1999 (first entry)

Borrelia burgdorferi polynucleotide sequence #35.

XX
KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
KW infection; diagnosis; characterisation; detection; ds.

OS Borrelia burgdorferi.

PN WO9858943-A1.

PD 30-DEC-1998.

XX 18-JUN-1998; 98WO-US12764.

XX 03-SEP-1997; 97US-0057483.

XX 20-JUN-1997; 97US-0050359.

XX 22-JUL-1997; 97US-0053344.

XX 22-JUL-1997; 97US-0053377.

(HUMA-) HUMAN GENOME SCI INC.

(MEDI-) MEDIMMUNE INC.

XX Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;

PI White OR;

XX WPI; 1999-081217/07.

XX New isolated Borrelia burgdorferi nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention
PT and therapy of infections, particularly Lyme disease

XX Claim 1; Page 998-1000; 1128pp; English.

XX AAX20248 to AAX20402 represent polynucleotide sequences isolated from
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for
CC the detection, diagnosis, characterisation, prevention and therapy of
CC Bb infections, e.g. Lyme disease. They can also be used for the
CC production of biosynthetic products, e.g. enzymes. Borrelia belongs
CC to a family of motile, spiral-shaped bacteria called Spirochetes.
CC Spirochetes are pathogenic in humans and Borrelia causes epidemic and
CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
CC Lyme disease.

SQ Sequence 3398 BP; 1096 A; 535 C; 869 G; 896 T; 2 other;

Query Match 34.3%; Score 204; DB 20; Length 3398;

Best Local Similarity 62.5%; Pred. No. 4.7e-22;

Matches 385; Conservative 0; Mismatches 200; Indels 31; Gaps 3;

QY 1 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAACATACACTACTACTGCTTAGGATCGGA 60

Db 2995 GTACCGCTTTAAATAGGCGAACAGCCATACCTTTAGGACCTGCTCCAGCCCTTAGGATCGGA 2936

QY 61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAGATTAGCC 120

Db 2935 TGAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAGATTAGCC 2876

QY 121 TGTATCCCTAGAGTAAGTATTTTATCCGTTAAGCGGATAATTTTATTAATAATTAATATCG 180

Db 2875 TGTATCCCGGAGTACCTTTTATTCGTTAAGTCAGCGGCTTCCACT-TGCCACCGCCA 2817

QY 181 GATCATTAAAGCCGACATTAATCTCTGTTAAATTTGTAATTTTACAGTTAATATATAT 240

Db 2816 GATCATTAAAGCCGACATTTTCGATCTCTGCTGATCTGTCAGTCTTACAGTTAAGTACCTT 2757

QY 241 TTATCTTTA-----TATAATAATAATAATAATTTTATTAATAATAATATCG 278

Db 2756 ATGCCCTTTACACTTACAGATGATTTCCAAACCACTCTAAGGTAACCTTTGGCACCTCCG 2697

QY 279 TTTTATATAGGAGAGACGCCAGTCAAACTATCTTATAAATATCTTAAAAATTTT 338
DB 2696 TTACTCTTTAGGAGGCGACGCCAGTCAAACTACCCAGCTCTCTCATATTT 2637
QY 339 GTTATAAAATTTTATAAGAATTTTATATATATATAAATGGTATTTCAATTAACAATTACA 398
DB 2636 CT-----ATAAGTTAGAAACCTAAATTAACAAGGTTGGTATTTCGAAGATTGACTCCA 2585
QY 399 TTATTTCCAAAATAATATTAATCTACTTCCCATTTATCTATGTTATATATATATATTT 458
DB 2584 CTACCCCTGACGAGATAGCTTCAAGTCTCCACCTATCTACACATATTTTAATCAAAATC 2525
QY 459 TCAATATCTTATTAATAGTAAAGCTTCATAGGGTCTTTCTGTCTCTATATAAAGAAATCTGC 518
DB 2524 TCAATACCAAGCTATAGTAAAGTTACAGGGTCTTTCCGTCTAACCACAAGTAAATCGGC 2465
QY 519 ATCTTCACAGATAATTTTATTTCAATTAAGATTTTATTAAGCAGCATTTAAGTCGTTAC 578
DB 2464 ATCTTCACGATACCTCAATTTACCGAGCTCCACGTTGAGACAGGTCCTCAAAATCGTTAC 2405
QY 579 ATCTTTCAATGACAGTTC 594
DB 2404 ACCATTCTGCGGGTC 2389

RESULT 3
AAH54997
ID AAX20249 standard; DNA; 116277 BP.
XX
AC AAX20249;
XX
DT 04-MAY-1999 (first entry)
XX
DE Borrelia burgdorferi polynucleotide sequence #2.
XX
KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
KW infection; diagnosis; characterisation; detection; ds.
XX
OS Borrelia burgdorferi.
XX
PN WO9858943-Al.
XX
PD 30-DEC-1998.
XX
PF 18-JUN-1998; 98WO-US12764.
XX
PR 03-SEP-1997; 97US-0057483.
PR 20-JUN-1997; 97US-0050359.
PR 22-JUL-1997; 97US-0053344.
PR 22-JUL-1997; 97US-0053377.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMUNE INC.
XX
PI Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;
PI White OR;
XX
DR WPI; 1999-081217/07.
XX
PT New isolated Borrelia burgdorferi nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention
PT and therapy of infections, particularly Lyme disease
XX
PS Claim 1; Page 672-737; 1128pp; English.
XX
CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for
CC the detection, diagnosis, characterisation, prevention and therapy of
CC Bb infections, e.g. Lyme disease. They can also be used for the
CC production of biosynthetic products, e.g. enzymes. Borrelia belongs
CC to a family of motile, spiral-shaped bacteria called Spirochetes.

CC Spirochetes are pathogenic in humans and Borrelia causes epidemic and
CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
CC Lyme disease.
XX
SQ Sequence 116277 BP; 42656 A; 19868 C; 14490 G; 39250 T; 13 other:
Query Match 34.3%; Score 204; DB 20; Length 116277;
Best Local Similarity 62.5%; Pred. No. 3.1e-22;
Matches 385; Conservative 0; Mismatches 200; Indels 31; Gaps 3;
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DB 80067 GTACCCCTTTAAATGGCGAACGCCATACCTTTAGGACCTGCTCCAGCCCTAGGATGCGA 80126
QY 61 TAAGCCGACATCGAGGTGCGCAACCTTTTCGTCGAATATGACATCTCGGAAAGATTAAGCC 120
DB 80127 TGAGCCGACATCGAGGTGCGCAACCTTTTCGTCGATGTGAATCTTTGGGAAGGTAAAGCC 80186
QY 121 TGTATTCCTTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTTATTAATAATTAATCG 180
DB 80187 TGTATTCCTTAGAGTAACCTTTTATTCGTTAAGTGACGGCGCTTCCACT-TGCCACCGCCA 80245
QY 181 GATCATTAAGACGACATTAATCTCTGTTAAATTTGTAATTTTACAGTTAATATATAT 240
DB 80246 GATCACTAAGACCTACTTTCGTTATCTGTTCCGACTTGTCACTTTACAGTTAAGCTACCTT 80305
QY 241 TTATCTTTA-----TATAATAATAATAACATTTGTACACCTCG 278
DB 80306 ATGCCCTTTACACTTACAGAGTGATTTCCAACTCTTAAGGTAACTTTTGGCGACCTCG 80365
QY 279 TTTTATATAGGAGAGACGCCAGTCAAACTATCTTATAAATATTTGTTAAAAATTTT 338
DB 80366 TTACTCTTTAGGAGGCGACGCCAGTCAAACTACCCAGCTCTCTCATATTT 80425
QY 339 GTTATAAAATTTTATAAGAATTTTATATATATATAAATGGTATTTCAATTAACAATACA 398
DB 80426 CT-----ATAAGTTAGAAACCTAAATTAACAGAGGTGGTATTTCAAGATTGACTCCA 80477
QY 399 TTATTTCCAAAATAATATTAATTAATCTACTTCCCATTTTCTATGTTATATATATATATTT 458
DB 80478 CTACCCCTGACGAGATAGCTTCAAAGTCTCCACCTATCCGACACATATTTAATCAATC 80537
QY 459 TCAATATCTTATAAGTAAAGCTTCATAGGGTCTTTCTGCTCTAATAATAAGAAATCTGC 518
DB 80538 TCAATACCAAGCTATAGTAAAGGTTCCAGGGGTCTTTCCGCTCTCAACCAAGTAATCGGC 80597
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DB 80598 ATCTTCACGATACCTTCAATTTTCAACGAGCTCCACGTTGAGACAGGTCCTCAATCGTTAC 80657
QY 579 ATCTTTCAATGACAGTTC 594
DB 80658 ACCATTCTGCGGGTC 80673

RESULT 4
AAH54997
ID AAX54997 standard; DNA; 1385 BP.
XX
AC AAX54997;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4361.
XX
KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.


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Db 1421 ATCTTCACAGGTACTATGATTTCACCGAGTCTCTCGTTGAGACAGTCCCAAAATCGTTAC 1480
    |||||
QY 579 ATCTTTTCATGCGAGTC 594
    |||||
Db 1481 GCCTTCGTGCGGGTC 1496
    |||||

RESULT 7
ID AAH54319/C
XX AAH54319 standard; DNA; 3012 BP.
AC AAH54319;
DT 03-SEP-2001 (first entry)
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3683.
XX
KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
XX WO200134809-A2.
PN 17-MAY-2001.
PD
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX ) GLAXO GROUP LTD.
PI
PI Kimmerly WJ;
XX
XX WPI; 2001-316495/33.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 8; Page 1293-1294; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAG81454 to AAG8120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH5090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH5091 to
XX AAH5098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 3012 BP; 842 A; 612 C; 849 G; 709 T; 0 other;

Query Match 32.0%; Score 190; DB 22; Length 3012;
Best Local Similarity 59.7%; Pred. NO. 5.3e-20;
Matches 368; Conservative 0; Mismatches 225; Indels 23; Gaps 2;

QY 1 GTATCGCTTTAATAGGCGACAGACTTACCCCTTAAACATACACTACTGCGCTTAGGATGCGA 60
    |||
Db 2261 GTACCGCTTTAATGGGCGACAGCCCAACCCCTTGGGACCCACTACAGCCCGGATGCGA 2202
```

```
QY 61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAGATAGCC 120
    |||||
Db 2201 TGAGCCGACATCGAGGTGCCAAACCTCCCGCTCGATGTGAACCTCTTGGGGGAGATAGCC 2142
    |||||
QY 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATATATTAATAATTATCG 180
    |||||
Db 2141 TGTATCCCGGGGTAGCTTTTATCCGTTGAGCGATGGCCCT-TCCATGCGGAACACCG 2083
    |||||
QY 181 GATCATTAAAGACCGACATTAATCTCTCTTTAAATTTTAAATTTTACAGTTTAAATATATAT 240
    |||||
Db 2082 GATCATAAGTCCGCTCTTTCGACCCCTCTCGACTTGTAGGCTCGCAGTCAAGCTCCCTT 2023
    |||||
QY 241 TTATCTTTATATAATAATAT- - - - -AACATTTGACACCTCCG 278
    |||||
Db 2022 ATGCCTTTACACTCTATGAATGATTTCCAAACCATTTCTGAGGGAACCTTTGAGCGCCTCCG 1963
    |||||
QY 279 TTTTATATAGGAGGAGACCGCCCGCCAGTCAAACTATCTTATAAATATTTTAAAAATTTT 338
    |||||
Db 1962 TTACCTTTTATAGGAGCGACCGCCCGCCAGTCAAACTGCGCCGCTGACACTGTCTCCCAAC 1903
    |||||
QY 339 GTTATAAAAAATTTTATAAGAAATTTATATATATAATAAATGATTTTCAATTAACAATATACA 398
    |||||
Db 1902 GATAAGTGGTGGGGTTAGAAAGCCACACAGCTAGGGTAGTATCCCAACCAACGCTCCA 1843
    |||||
QY 399 TTATTTCCAAAAAATAATATTAATTAATCTTCCCAATTTTATCTATGTTATATATATATATTT 458
    |||||
Db 1842 CGTAAGCTAGCGCTCAGCTTTGAAAGGCTCCTACCTATCTGTACAAAGCTGTGCGGAATT 1783
    |||||
QY 459 TCAATATCTAATAAGCTTTCATAGGCTTTCATAGGCTCTTTCTGCTCCTAATAATAAGAATCTGC 518
    |||||
Db 1782 TCAATATCAGGCTACAGTAAAGCTCCACGGGCTCTTTCCGCTCTGCGGGTAACCTGC 1723
    |||||
QY 519 ATCTTCACAGATAATTTTATTTTCAATTAAGATTTTTTTTAAAGACAGCATTTTAAAGTCGTTAC 578
    |||||
Db 1722 ATCTTCACAGTACTATGATTTTCAACGAGTCTCTCGTTGAGACAGTCCGCAATCGTTAC 1663
    |||||
QY 579 ATCTTTTCATGCGAGTC 594
    |||||
Db 1662 GCCTTTCTGCGGGTC 1647

RESULT 8
AAH54343
ID AAH54343 standard; DNA; 3012 BP.
XX
AC AAH54343;
XX
XX 03-SEP-2001 (first entry)
DT
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3707.
XX
XX Staphylococcus epidermidis SRI strain; infection; diagnosis;
XX vaccination; endocarditis; ds.
XX
XX Staphylococcus epidermidis.
XX
XX WO200134809-A2.
XX
XX 17-MAY-2001.
PD
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Kimmerly WJ;
XX
XX WPI; 2001-316495/33.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX
```


Claim 8; Page 1323-1324; 2188pp; English.

Claim 8; Page 1323-1324; 2188pp; English.

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG81320, from *Staphylococcus epidermidis*. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the *S. epidermidis* polypeptides (II) via the production of vectors containing them which are used to produce host cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed *S. epidermidis* genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472 no sequences are present for SEQ ID NO:4455 to 4464.

Sequence 3012 BP; 692 A; 887 C; 653 G; 780 T; 0 other:

Query Match 32.0%; Score 190; DB 22; Length 3012;
Best Local Similarity 59.7%; Pred. No. 5.3e-20;
Matches 368; Conservative 0; Mismatches 225; Indels 23

<p>est. bootstrap Matches</p>	<p>Similarity 368; Conservative</p>	<p>File: NO. 3.3E-20; Mismatches 225;</p>	<p>Indels 23; Gaps</p>
QY	1	GTAATCGCTTTAATAGGGCAACAGACTTACCCTTAAACATCATCTACTGCTTAGGATGGGA	60
DB	942	GTACCGCTTTAATGGGGAACAGCCAACCCCTTGGGACCGACTACAGCCCAGGATGCGA	1001
QY	61	TAAAGCCAGATCGAGGTGCCAAACGTTTTTCGTCRAATATGGACTCTCGGAAAGAATTAGCC	120
DB	1002	TGAGCCGACATCGAGGTGCCAAACCTCCCGTCGATGTGAATCTCTTGCGGGGAGATAAGCC	1061
QY	121	TGTTATCCCTAGACTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAAATTATCG	180
DB	1062	TGTTATCCCCGGGTAGCTTTTATCCGTTGAGCAGATGCCCT-TCCATGCGGAACCAACG	1120
QY	181	GATCAATTAAGACCGACATTAATCTCTGTTTAAATTTGTATAAATTTTACAGTTAAATTATAT	240
DB	1121	GATCACATAAGTCCCTCTTTTCGACCCCTGCTGCACCTTGAGGTCTCGCAGTCAAGCTCCCTT	1180
QY	241	TTATCTTTTATATAATAATAT-----RACATTGTACACCTCCG	278
DB	1181	ATGCCTTTACACTCTATGAATGATTTCCAACCATTCGAGGGAACTTTGAGCGCTCCG	1240
QY	279	TTTTTATATAGGAGGACCGCCCGAGTCAAACHATCTTATAAATATTGTAAAAATTTT	338
DB	1241	TTACCTTTTAGGAGGCGACCGCCCGAGTCAAACCTGCCGCGCTGCACGTCTCCCAACCAC	1300
QY	339	GTTATAAAAATTTTATAGAAATTTATATATATAAANAATGTTATTTCAATAACAATTACA	398
DB	1301	GATAAGTGTGCGGGTTAGAAAGCCAACAGCAGTGGGTAGTATCCCAACCAAGCGCTCCA	1360
QY	399	TTATTTCCAAAAAATAATATTACTCTCCCATTTATCTATGTTATATATATATATT	458
DB	1361	CGTAAGCTAGCGCTACGTTTTCAAAGGCTCCTACCTATCCTGTACAAGCTGTGCGGAAT	1420
QY	459	TCAATATCTAATATAGTAAGACTTCATAGGGCTTCTGTCTTCTTAATAATAGAANAATCGC	518
DB	1421	TCAATATACAGCTACAGTAAGACTTCCAGGGGGTCTTCCCGTCTGTCCGGGGTAACCTGC	1480
QY	519	ATCTTCACAGATAATTTATTTTCATTAAGATTTTTTTTAAAGACAGCATTTTAAAGTCGTTAC	578
DB	1481	ATCTTCACAGTACTATGATTTTACCNGTCTCTCGTTGACACAGTGCCCAANATCGTTAC	1540
QY	579	ATCTTTTCATGAGTGC	594
DB	1541	GCCTTTTCGTGCGGTC	1556

RESULT 9

AAH54552	
ID	AAH54552 standard; DNA; 3030 BP.
XX	
XX	
XX	AAH54552;
XX	
DT	03-SEP-2001 (first entry)
XX	
XX	
DE	S. epidermidis genomic polynucle
XX	
KW	Staphylococcus epidermidis SR1 s
KW	vaccination; endocarditis; ds.
XX	
XX	
OS	Staphylococcus epidermidis.
XX	
PN	WO200134809-A2.
XX	
PD	17-MAY-2001.
XX	
XX	
PF	09-NOV-2000; 2000WO-US30782.
XX	
PR	09-NOV-1999; 99US-0164258.
XX	
PA	(GLAX) GLAXO GROUP LTD.
XX	
PI	Kimmerly WJ;
XX	
DR	WPI; 2001-316495/33.

Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*, useful for vaccinating against infections, e.g. endocarditis -

Claim 8; Page 1571-1572; 2188pp; English.

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AA811454 to AA831210, from *Staphylococcus epidermidis*. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the *S. epidermidis* polypeptides (II) via the production of vectors containing them which are used to produce hosts' cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed *S. epidermidis* genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.

Sequence 3030 BP; 918 A; 678 C; 519 G; 915 T; 0 other;

ery Match 32.0%; Score 190; DB 22; Length 3030;
st Local Similarity 59.7%; Pred. No. 5.3e-20;

Seq. local similarity	Seq. id.	Indels	Mismatches	Indels	Gaps
368; Conservative	0; Mismatches	225;			
				23;	2;

Qy	1	GTATCGCTTTAATAGCGGAACAGACTTACCCCTTAAACATACTACTGCTTTAGGATCGCA	60
Db	2225	GTACCGCTTTAATGGCGAACAGCCCAACCTTTGGAGCGGACTACAGCCCCAGGATGCGA	2284
Qy	61	TAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAGAGTATGCC	120
Db	2285	TGAGCCGACATCGAGGTGCCAAACCTCCCGTCGATGTGAACCTCTGGGGAGATAAGCC	2344
Qy	121	TGTTATCCCTAGAGTAACTTTTATCGGTTAAGCGGATAATTTTATTATTAATAATATATCG	180
Db	2345	TGTTATCCCGGGGTAGCTTTTATCCGTTAGACGATGGCCCT-TCATGTGGGAACCAACCG	2403

Db 1388 GATAAGTGTGGGGTTAGAAAGCCAAACACAGCTAGGGTAGTATCCCAACGCTCCA 1447
 QY 399 TTATTTCCAAAATAATATTACTTCCCATTTATTCCTATGTTATATATATATATTT 458
 Db 1448 CTAAGCTAGCGCTCAGGTTTCAAGGCTTCCACCTATCTGTACAGGTGCGGAAT 1507
 QY 459 TCAATATCTATTATAGTAAAGCTTCATAGGCTCTTCTGTCTCTAATAAAGAAATCTGC 518
 Db 1508 TCAATATCAGGCTACAGTAAAGCTCCAGGGGTCTTTCGGTCTGTGCGGGGTACCTGC 1567
 QY 519 ATCTTCACAGATAATTTATTTCAATAGATTTTTTTTAAAGACAGCATTTAAGTGTATC 578
 Db 1568 ATCTTCACAGTACATGATTTTCAAGGCTCTCTGTGTGAGACAGTGGCCAAATCGTTAC 1627
 QY 579 ATCTTTTCATGCAAGTTC 594
 Db 1628 GCCTTTCGTGCGGGTC 1643

RESULT 14
 AAH54539/c

ID AAH54539 standard; DNA: 3405 BP.

XX AAH54539;

AC AAH54539;

DT 03-SEP-2001 (first entry)

DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3903.

XX Staphylococcus epidermidis SRI strain; infection; diagnosis;

KW vaccination; endocarditis; ds.

XX Staphylococcus epidermidis.

OS WO200134809-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30782.

XX 09-NOV-1999; 99US-0164258.

XX (GLAX) GLAXO GROUP LTD.

FA Kinmerly WJ;

PI WPI; 2001-316495/33.

DR Nucleic acids encoding polypeptides from Staphylococcus epidermidis,

XX useful for vaccinating against infections, e.g. endocarditis -

PS Claim 8; Page 1556-1557; 2188pp; English.

XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,

CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX
 SQ Sequence 3405 BP; 971 A; 670 C; 922 G; 842 T; 0 other;
 Query Match 32.0%; Score 190; DB 22; Length 3405;
 Best Local Similarity 59.7%; Pred. No. 5.2e-20;
 Matches 368; Conservative 0; Mismatches 225; Indels 23; Gaps 2;
 QY 1 GTATCGCTTAATAGCGCAACAGCTTACCCCTTAAACATACATACTGCTTACCTAGGATGCA 60
 Db 2171 GTACCGCTTAATAGCGCAACAGCTTACCCCTTAAACATACATACTGCTTACCTAGGATGCA 2112
 QY 61 TAAGCGCATCGAGGTGCAAAACCTTTTCGTCATATGAGCTCTCGGAAAGATTAGCC 120
 Db 2111 TGAGCGCATCGAGGTGCAAAACCTTCCCGTCGATGTGAACCTTTGGGGAGATAAGCC 2052
 QY 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATTAATATG 180
 Db 2051 TGTATCCCGGGGTAGCTTTTATCCGTTGAGCGATGGCCCT-TCCATCGGAACACCG 1993
 QY 181 GATCATTAAGACCGACATTAATCTCTGTTTAAATTTTAAATTTTACAGTTAATATATAT 240
 Db 1992 GATCATAAGTCCGCTTTTCGACCCCTGCTCGACTGCTCGAGTCAAGCTCCCTT 1933
 QY 241 TTATCTTTATATAAATAATAT-----AACATTGTACACTCG 278
 Db 1932 ATGCTTTTACACTCTATGAATGATTTCCAAACCATTTCTGAGGGAACCTTTGAGCGCTCG 1873
 QY 279 TTTTATATAGGAGAGACCGCCCGCAGTCAAACTATCTTATATAATTTTAAAAATTT 338
 Db 1872 TTACCTTTTAGGAGCGACCGCCCGCAGTCAAACTGCCCCCTGACACTGTCTCCACCAC 1813
 QY 339 GTTATAAAAAATTTTATAAGAAATTTATATATATAAATGTTATTCATTACAAATACA 398
 Db 1812 GATAAGTGTGCGGGTTAGAAAGCCAAACACAGCTAGGTTAGTATCCCAACACCGCTCCA 1753
 QY 399 TTATTTTCCAAAAAATAATATTACTTCCCATTTTATCTATGTTATATATATATATTT 458
 Db 1752 CGTAAGCTAGCGCTCAGCTTTTCAAGGCTCCTACCTATCTGTACAGCTGTCCGAAT 1693
 QY 459 TCAATATCTATTAAATAGTAAAGCTTCATAGGCTCTTTCTGCTCTATATATAAGAAATCTGC 518
 Db 1692 TCAATATCAGGCTACAGTAAAGCTCCAGGGGTCTTTCCGCTCTGTGCGGGTAAACCTGC 1633
 QY 519 ATCTTCACAGATAATTTTATTTTCAATTAAGATTTTTTTTAAAGACAGCATTTAAGTCTGTTAC 578
 Db 1632 ATCTTCACAGTACTATGATTTTCAAGGAGTCTCTCGTTGAGACAGTGGCCAAATCGTTAC 1573
 QY 579 ATCTTTTCATGCAAGTTC 594
 Db 1572 GCCTTTCGTGCGGGTC 1557

RESULT 15

AAH54518/c

ID AAH54518 standard; DNA; 3500 BP.

XX AAH54518;

XX 03-SEP-2001 (first entry)

XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3882.

XX Staphylococcus epidermidis SRI strain; infection; diagnosis;

XX vaccination; endocarditis; ds.

XX Staphylococcus epidermidis.

OS WO200134809-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30782.

XX 09-NOV-1999; 99US-0164258.
XX PA (GLAX) GLAXO GROUP LTD.
XX PI Kimmerly WJ;
XX DR WPI; 2001-316495/33.

XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
PT
XX

PS Claim 8; Page 1530-1532; 2188pp; English.

XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.

XX Sequence 3500 BP; 980 A; 712 C; 1004 G; 804 T; 0 other;

Query Match 32.0%; Score 190; DB 22; Length 3500;
Best Local Similarity 59.7%; Pred. No. 5.2e-20;
Matches 368; Conservative 0; Mismatches 225; Indels 23; Gaps 2;

QY 1 GTATCGCTTTAATAGGGGAACACACTTACCTTTAAACATACACTACTGCTTAGGATGCGA 60
DB 3383 GTACCGCTTTAATAGGGGAACACCCCTTTGGGACCGACTACAGCCCGAGGATGCGA 3324
QY 61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCATATGACTCTCGGAAAGATTAGCC 120
DB 3323 TGAGCCGACATCGAGGTGCCAAACCTTCCCGTCGATGTGAATCTTTGGGGGAGATAAGCC 3264
QY 121 TGTATCCCTAGAGTAACCTTTTATCGTTAAGCGATAATTTTATTATTAAATAATTATCG 180
DB 3263 TGTATCCCGGGGTAGCTTTTATCGTTGAGCGATGGCCCT-TCCATCGGGAACCCACCG 3205
QY 181 GATCATTAAAGACCGCATTAATCTCTGTTTAATTTGCTAAATTTACAGTTAATTATATAT 240
DB 3204 GATCATTAAAGTCCGCTTTTCGACCCCTGCTCGACTTGTAGGCTCTCGGAGTCAAGCTCCCTT 3145
QY 241 TTATCTTTTATATAATAATAT-----AACATTGTACACCTCCG 278
DB 3144 ATGCCCTTACACTCTATGAATGATTTCCAAACCATTTCTGAGGGAACCTTTGAGGCGCTCCG 3085
QY 279 TTTTATATAGGAGGACCGCCCAAGTCAAACTATCTTTATATAATATGTTAAAAATTTT 338
DB 3084 TTACCTTTTAGGAGGCGACCGCCCAAGTCAAACTGCGCCCTGACACTGTCTCCACCAC 3025
QY 339 GTTATAAAATTTTATAAGNATTTATATATATAATAAATGGTATTTCATTAAACAATTACA 398
DB 3024 GATAAGTGGTGGGGTTAGAAAGCCCAACACAGCTAGGGTAGTATCCCAACCGCTCCA 2965
QY 399 TTATTTCCAAAAAATAATATTAATACTACTTCCCATTTTATCTTATGTTATATATATATAT 458
DB 2964 CGTAAGCTAGCGCTACGGTTTCAAGGCTTCTTACCTATCTGTACAAAGCTGTGCCGAAT 2905

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OM nucleic - nucleic search, using sw model

Run on: October 17, 2002, 10:11:59 : Search time 1849 seconds
(without alignments)
6722.749 Million cell updates/sec

Title: US-09-369-992c-1_copy_1147_1740
Perfect score: 594
Sequence: 1 gtagctttaaaggcgaa.....ttacatcttccagcagtc 594

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Query Match Length DB ID Description

SUMMARIES

1	594	100.0	5849	3	PBU79731	U79731 Plasmodium
2	578	97.3	594	3	AF182847	AF182847 Plasmodium
c	557.2	93.8	594	3	PVU97561	PVU97561 Plasmodium
4	554	93.3	594	3	AF182846	AF182846 Plasmodium
c	552.4	93.0	594	3	PVU97562	PVU97562 Plasmodium
c	546.8	92.1	593	3	PVU97565	PVU97565 Plasmodium
c	543	91.4	2700	3	PFLSRN	X61660 Plasmodium
c	543	91.4	5142	3	PFLSRN	X75545 P.falciparu
c	543	91.4	15421	3	PFCOMPRA	X95275 P.falciparu
c	541.4	91.1	595	3	PVU97558	PVU97558 Plasmodium
c	539.8	90.9	595	3	PVU97558	PVU97558 Plasmodium
c	532.6	89.7	594	3	PVU97559	PVU97559 Plasmodium
c	532	89.6	596	3	PVU97564	PVU97564 Plasmodium
c	530.4	89.3	596	3	PVU97563	PVU97563 Plasmodium
c	528.6	89.0	595	3	PVU97557	PVU97557 Plasmodium
c	512	86.2	598	3	PVU97556	PVU97556 Plasmodium
c	497	83.7	2621	3	PVU9732	U79732 Plasmodium
c	256.8	43.2	73345	8	ALO294725	AJ294725 Astasia 1
c	254	42.8	7291	1	AF211133	AF211133 Carsonell
c	252.6	42.5	34996	3	U87145	U87145 Toxoplasma
c	252.6	42.5	34996	3	U87145	U87145 Toxoplasma
c	249.4	42.0	2700	3	AF304316	AF304316 Neospora
c	249.4	42.0	7847	3	AF304319	AF304319 Neospora
c	249.2	42.0	6717	1	AF211135	AF211135 Carsonell
c	248.6	41.9	3269	3	AF304322	AF304322 Neospora
c	246.8	41.5	6730	1	AF211134	AF211134 Carsonell
c	242	40.7	5087	1	AF211143	AF211143 Carsonell
c	241.2	40.6	6113	3	TGTRNARRN	Y11430 T.gondii pl
c	240.8	40.5	3983	1	AF211144	AF211144 Carsonell
c	239.2	40.3	3987	1	AF211145	AF211145 Carsonell
c	236.2	39.8	164921	8	AF022186	AF022186 Cyanidium
c	235.6	39.7	7347	1	AF211124	AF211124 Carsonell
c	233.6	39.3	3985	1	AF280097	AF280097 Carsonell
c	233.6	39.3	3988	1	AF243137	AF243137 Carsonell
c	233.6	39.3	4569	1	AF211151	AF211151 Carsonell
c	232.4	39.1	7806	1	AF211141	AF211141 Carsonell
c	232	39.1	3986	1	AF211136	AF211136 Carsonell
c	232	39.1	3990	1	AF243138	AF243138 Carsonell
c	232	39.1	3996	1	AF211129	AF211129 Carsonell
c	232	39.1	4022	1	AF211148	AF211148 Carsonell
c	231.6	39.0	2957	8	CHPLIB	X61179 P.littoralis
c	230.4	38.8	3987	1	AF243136	AF243136 Carsonell
c	230.4	38.8	3995	1	AF211125	AF211125 Carsonell
c	230.4	38.8	3998	1	AF211130	AF211130 Carsonell
c	228.8	38.5	3992	1	AF211131	AF211131 Carsonell

ALIGNMENTS

RESULT 1
PBU79731
LOCUS
DEFINITION
Plasmodium berghei extrachromosomal plasmid PB-1, ORF470 gene, partial cds, tRNA-Thr, large subunit ribosomal RNA, tRNA-Met, tRNA-Arg, tRNA-Val, tRNA-Arg, tRNA-Leu, tRNA-Ala, tRNA-Ala, and small subunit ribosomal RNA genes, complete sequences.
U79731
U79731.1 GI:2662401
Plasmodium berghei.
Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
REFERENCE
AUTHORS
Yap,M.W., Kara,U.A., ten Heggeler-Bordier,B., Ting,R.C. and Tan,T.M.
TITLE
Partial nucleotide sequence and organisation of extrachromosomal plasmid-like DNA in Plasmodium berghei
JOURNAL
MEDLINE
Gene 200 (1-2), 91-98 (1997)
REFERENCE
AUTHORS
2 (bases 1 to 5849)
Yap,M.W.C., Kara,U.A.K. and Tan,T.M.C.
TITLE
Direct Submission

JOURNAL Submitted (26-NOV-1996) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore

FEATURES
source Location/Qualifiers
1..5849
/organism="Plasmodium berghei"
/strain="ANKA"
/db_xref="taxon:5821"
/note="extrachromosomal plasmid PB-1"
complement(<1..711)
/note="ORF470"
/codon_start=1
/protein_id="AAB88271.1"
/db_xref="GI:2662402"
translation="MINKLKLKFLNLYNKKYNNKINLYLRNGLNKLKLNLS
NNIYLFFPKFYKLSLKLNFKLDWSECFPCNLSYDNIYYSTLKDLSNLLYLR
TNLNFIDYFNKLIPIIDVICDSISVLHTQYFLKLGILFSLDLVILKPLVLR
KYLGVVYKDNFNFANISIIIFSEGSFYVSKYIKGSPNLSYFKTNSYDFAQFERTL
LIASEFAYGVLEGCTASL"
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/product="trna-Thr"
/product="trna-Thr"
complement(814..3521)
/product="large subunit ribosomal RNA"
complement(3565..3636)
/product="trna-Met"
complement(3646..3717)
/product="trna-Arg"
3742..3813
/product="trna-Val"
3817..3888
/product="trna-Arg"
3895..3975
/product="trna-Leu"
complement(3996..4058)
/product="trna-Asn"
4089..4159
/product="trna-Ala"
4208..5648
/product="small subunit ribosomal RNA"
5793..5849
/product="trna-Ile"

BASE COUNT 2296 a 673 c 557 g 2323 t

Query Match 100.0%; Score 594; DB 3; Length 5849;
Best Local Similarity 100.0%; Pred. No. 4,1e-73;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACATACTACTGCGCTTAGGATGCGA 60
Db 1147 GTATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACATACTACTGCGCTTAGGATGCGA 1206

Qy 61 TAAGCCGACATCGAGTGCACAAACCTTTTCGTCGAATATGGACTCTCGGAAAGATTAGCC 120
Db 1207 TAAGCCGACATCGAGTGCACAAACCTTTTCGTCGAATATGGACTCTCGGAAAGATTAGCC 1266

Qy 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAAATTTTATTAATAAATATATCG 180
Db 1267 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAAATTTTATTAATAAATATATCG 1326

Qy 181 GATCATTAAAGACCGACATTAATCTCTGTTTAAATTTTGTAAATTTTACAGTTAAATATATAT 240
Db 1327 GATCATTAAAGACCGACATTAATCTCTGTTTAAATTTTGTAAATTTTACAGTTAAATATATAT 1386

Qy 241 TTATCTTTATATATAAATAATACATGTACACCTCGGTTTTTATATAGGAGGAGACCGC 300
Db 1387 TTATCTTTATATATAAATAATACATGTACACCTCGGTTTTTATATAGGAGGAGACCGC 1446

Qy 301 CCCAGTCAAACTACTCTTATAAATATTTGTTAAAAATTTTGTATAAAAAATTTTATAAGAAT 360
Db 1447 CCCAGTCAAACTACTCTTATAAATATTTGTTAAAAATTTTGTATAAAAAATTTTATAAGAAT 1506

Qy 361 TTATATATATATAAATAGGTATTTTCATTAACAATTAATTTTCCAAAAAATAATATT 420

Db 1507 TTATATATATAAATAGGTATTTTCATTAACAATTAATTTTCCAAAAAATAATATT 1566

Qy 421 ACTACTTCCCATTTATTTCTATGTTATATATATATATATTTTCAATATCTATTAATAGTAAAG 480

Db 1567 ACTACTTCCCATTTATTTCTATGTTATATATATATATATTTTCAATATCTATTAATAGTAAAG 1626

Qy 481 CTTTCATAGGCTCTTCTGCTCTAATAAAGAAATCTGCATCTTCACAGATAAATTTTATTT 540

Db 1627 CTTTCATAGGCTCTTCTGCTCTAATAAAGAAATCTGCATCTTCACAGATAAATTTTATTT 1686

Qy 541 CATTAAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTACATCTTTTCATGCAGGTC 594

Db 1687 CATTAAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTACATCTTTTCATGCAGGTC 1740

RESULT 2
AF182847
LOCUS
DEFINITION
Plasmodium chabaudi from Australia large subunit ribosomal RNA
AF182847
gene, partial sequence.
ACCESSION
AF182847
VERSION
AF182847.1 GI:6110458
SOURCE
Plasmodium chabaudi.
ORGANISM
Plasmodium chabaudi
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 594)
AUTHORS
Tham, J.N., Kohn, L.K. and Kara, A.U.K.
TITLE
Direct Submission
JOURNAL
Submitted (03-SEP-1999) Institute of Molecular and Cell Biology, 30
Medical Drive, Singapore 117609, Singapore
FEATURES
Location/Qualifiers
source
1..594
/organism="Plasmodium chabaudi"
/organelle="plastid"
/strain="adami DS"
/db_xref="taxon:5825"
/country="Australia"
<1..>594
/product="large subunit ribosomal RNA"

BASE COUNT 205 a 95 c 69 g 225 t

Query Match 97.3%; Score 578; DB 3; Length 594;
Best Local Similarity 98.3%; Pred. No. 1e-70;
Matches 584; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GTATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACATACTACTGCGCTTAGGATGCGA 60
Db 1 GTATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACATACTACTGCGCTTAGGATGCGA 60

Qy 61 TAAGCCGACATCGAGTGCACAAACCTTTTCGTCGAATATGGACTCTCGGAAAGATTAGCC 120
Db 61 TAAGCCGACATCGAGTGCACAAACCTTTTCGTCGAATATGGACTCTCGGAAAGATTAGCC 120

Qy 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAAATTTTATTAATAAATATATCG 180
Db 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAAATTTTATTAATAAATATATCG 180

Qy 181 GATCATTAAAGACCGACATTAATCTCTGTTTAAATTTTGTAAATTTTACAGTTAAATATATAT 240
Db 181 GATCATTAAAGACCGACATTAATCTCTGTTTAAATTTTGTAAATTTTACAGTTAAATATATAT 240

Qy 241 TTATCTTTATATATAAATAATACATGTACACCTCGGTTTTTATATAGGAGGAGACCGC 300
Db 241 TTATCTTTATATATAAATAATACATGTACACCTCGGTTTTTATATAGGAGGAGACCGC 300

Qy 301 CCCAGTCAAACTACTCTTATAAATATTTGTTAAAAATTTTGTATAAAAAATTTTATAAGAAT 360
Db 301 CCCAGTCAAACTACTCTTATAAATATTTGTTAAAAATTTTGTATAAAAAATTTTATAAGAAT 360

Qy 361 TTATATATATATAAATAGGTATTTTCATTAACAATTAATTTTCCAAAAAATAATATT 420

Db TTATATATATATAAATGGTATTTTCATTATTAATAATACATTATTTCCAAAAAATAATATC 420
 Qy 421 ACTACTTCCCATTATTCCTATGTTATATATATATATATATTTTCAATATCTATTAATAGTAAAG 480
 Db 421 AATACTTTCCCATTATTCCTATGTTATACATATATATTTTCAATACCTACTAATAGTAAAG 480
 Qy 481 CTTCATAGGGTCTTTCCTGCTCCTAATAAAGAAATCTGCATCTTCACAGATAATTTTATTT 540
 Db 481 CTTCATAGGGTCTTTCCTGCTCCTAATAAAGAAATCTGCATCTTCACAGATAATTTTATTT 540
 Qy 541 CATTAAGATTTTTTTTAAAGACAGCATTTAAGTCGTTACATCTTTTCATGCGAGTC 594
 Db 541 CATTAAGATTTTTTTTTTAAAGACAGCATTTAAGTCGTTACATCTTTTCATGCGAGTC 594

RESULT 3	
LOCUS	PVU97561/c
DEFINITION	Plasmodium vivax extrachromosomal plasmid large subunit ribosomal RNA gene, partial sequence.
ACCESSION	PVU97561
VERSION	U97561.1
KEYWORDS	GI:4100399
SOURCE	malaria parasite P. vivax.
ORGANISM	Plasmodium vivax
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS	Tan, T.M.C., Nelson, J.S., Ng, H.C., Ting, R.C.Y. and Kara, U.A.K.
TITLE	Direct PCR amplification and sequence analysis of extrachromosomal Plasmodium DNA from dried blood spots
JOURNAL	Acta Trop. 68 (1), 105-114 (1997)
MEDLINE	98013247
PUBMED	9352006
REFERENCE	2 (bases 1 to 594)
AUTHORS	Tan, T.M.C., Nelson, J.S., Ng, H.C., Ting, R.C.Y. and Kara, U.A.K.
TITLE	Direct Submission.
JOURNAL	Submitted (15-APR-1997) Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent S119260, Singapore

FEATURES	Location/Qualifiers
source	1. .594
	/organism="plasmodium vivax"
	/isolate="primary isolate pv12/p"
	/db_xref="taxon:5855"
	/note="extrachromosomal plasmid"
rRNA	<1. .>594
BASE COUNT	227 a 70 c 98 g 199 t
ORIGIN	

	Query Match	93.8%	Score 557.2;	DB 3;	Length 594;
	Best Local Similarity	96.1%;	Pred. No. 7.4e-68;		
	Matches 571;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;
QY	1	GTATCGCTTTAATAGGCGACAGACTTACCCCTTAAACATACTACTGCTTAGCATCGGA	60		
Db					
Db	594	GTATCGCTTTAATAGGCGACAGACTTACCCCTTAAACATACTACTGCTTAGCATCGGA	535		
QY	61	TAAGCCGACATCGAGGTGCGCAACCTTTTCGTCAAATATGGACTCTCGGAAAGATTAGCC	120		
Db					
Db	534	TAAGCCGACATCGAGGTGCGCAACCTTTTCGTCAAATATGGACTCTCGGAAAGATTAGCC	475		
QY	121	TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATATTAAATAATTATCG	180		
Db					
Db	474	TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATATTAAATAATTATCG	415		
QY	181	GATCATTAAAGACCCGACATTAACTCTCTGTTTAAATTTTACACAGTTAAATTTATATAT	240		
Db					
Db	414	GATCATTAAAGACCCGACATTAACTCTCTGTTTAAATTTTACACAGTTAAATTTATATAT	355		
QY	241	TTATCTTTTATATAATAATACATTTGTACCTCGTTTTTATATATAGGAGGAGACCGC	300		

Db	354	ATATCTTTATATACATATATAACATTTTGTA	CTCTCCGTTTTTTTATATATAGGAGGACCGC	295
Qy	301	CCAGCTAAACACTATCTTTATAAATATTTGTTAAAAAATTTTGTTATAAAAAATTTTATAAAGAAT	360	
Db	294	CCAGCTAAACACTATCTTTATAAATATCTGTTAAAAAATTTGTTAAAAAATTTTTTAAAGAAT	235	
Qy	361	TTATATATATATAAAAATGGGTATTTTCATTAACAATTAACATATTTTCCAAAAAATAATATT	420	
Db	234	TTATATATATAAAAATGGGTATTTTCATTTACAATTAACATATTTTCCAAAAAATAATATC	175	
Qy	421	ACTACTCTCCCAATTTATCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAAG	480	
Db	174	ATTATTTCCCAATTTATGCTATGCTCTATATATATATTTTCAATATCTATTCATAGTAAAG	115	
Qy	481	CTTCATAGGGCTTTCTGTCCTTAATAAAGAAATCTGCATCTTCACAGATAAATTTTATTT	540	
Db	114	CTTCATAGGGCTTTCTGTCCTTAATAAAGAAATCTGCATCTTCACAGATAAATTTTATTT	55	
Qy	541	CATTAAGATTTTTTTTAAAGACAGCATTTAAGTCGTTACATCTTTTCATGCGAGTC	594	
Db	54	CATTAAGATTTTTTTTAAAGACAGCATTTAAGTCGTTACATCTTTTCATGCGAGTC	1	
RESULT 4				
AF182846				
LOCUS		AF182846	594 bp	DNA linear INV 25-OCT-1999
DEFINITION		Plasmodium malariae from Burma large subunit ribosomal RNA gene, partial sequence.		
ACCESSION		AF182846		
VERSION		AF182846.1	GI:6110456	
KEYWORDS				
SOURCE		Plasmodium malariae.		
ORGANISM		Plastid Plasmodium malariae		
REFERENCE		Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
AUTHORS		1 (bases 1 to 594)		
TITLE		Tham,J.M., Khon,L.K. and Kara,A.U.K.		
JOURNAL		Submitted (03-SEP-1999), Institute of Molecular and Cell Biology, 30 Medical Drive, Singapore 117609, Singapore		
FEATURES		Location/Qualifiers		
source		1..594		
		/organism="Plasmodium malariae"		
		/organelle="plastid"		
		/strain="BTSH/104"		
		/db_xref="taxon:5858"		
		/country="Burma"		
		<1..>594		
rRNA		/product="large subunit ribosomal RNA"		
BASE COUNT	201 a	90 c	70 g	233 t
ORIGIN				
Query Match		93.3%	Score 554;	DB 3; Length 594;
Best Local Similarity		95.8%	Pred. No. 2e-67;	
Matches 569;	Conservative	0;	Mismatches 25;	Indels 0; Gaps 0;
Qy	1	GTATCGCTTTAATAGCGCAACAGACTTACCCCTAAAAACATACTACTGCTTAGGATCGCA	60	
Db	1	GTATCGCTTTAATAGCGCAACAGACTTACCCCTAAAAACATACTACTGCTTAGGATGTA	60	
Qy	61	TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGCACCTCGGAAAAAGATTAGCC	120	
Db	61	TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGCCTCGGAAAAAGATTAGCC	120	
Qy	121	TGTTATCCCTAGACTACTTTTATCCGTTAAGCGATAATTTTATATTAATAATATATCG	180	
Db	121	TGTTATCCCTAGACTACTTTTATCCGTTAAGCGATAATTTTATATTAATAATATATCG	180	
Qy	181	GATCATTTAAGACCCGACATTAATCTCTCTTTAAATTTTGAAAAATTTTACAGTTAAATATATAT	240	
Db	181	GATCATTTAAGACCCGACATTAATCTCTCTTTAAATTTTGAAAAATTTTACAGTTAAATATATAT	240	
Qy	241	TTATCTTTATATAATAATAATACATTTGTACACCTCCGTTTTTATATAGGAGGACCGC	300	

Db 241 ATATCTTTTATAATAAATAAACAATTGTACTCTCTCGTTTATATATATAGGAGGAGCCGC 300
QY 301 CCAGTCAAACTATCTTATAAATATTTGTTAAATAATTTGTTATAAATAATTTTATAAGAAT 360
Db 301 CCAGTCAAACTATCTTATAAATATTTGTTAAATAATTTGTTATAAATAATTTTATAAGAAT 360
QY 361 TTATATATATAAATAAATGTTATTTTCAATTAACAATACATTTTCCAAAAATAATATT 420
Db 361 TTATATATATAAATAAATGTTATTTTCAATTAACAATACATTTTCCAAAAATAATATT 420
QY 421 ACTACTTCCCAATTTATCTATGTTATATATATATTTTCAATTAACAATACATTTTATAAGTAAAG 480
Db 421 TATATTTCCCAATTTATCTATGTTATATATATATTTTCAATTAACAATACATTTTATAAGTAAAG 480
QY 481 CTTCATAGGGCTTTCTGCTCTAATAAAGAAATCTGCATCTTCACAGATAATTTTATT 540
Db 481 CTTCATAGGGCTTTCTGCTCTAATAAAGAAATCTGCATCTTCACAGATAATTTTATT 540
541 CATTAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTACATCTTTTCATGCAGGTC 594
Db 541 CATTAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTACATCTTTTCATGCAGGTC 594

RESULT 5
PVU97562/c
LOCUS
DEFINITION
Plasmodium vivax extrachromosomal plastid large subunit ribosomal
RNA gene, partial sequence.
ACCESSION
U97562
VERSION
U97562.1
KEYWORDS
GI:4100400
SOURCE
malaria parasite P. vivax.
ORGANISM
Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 594)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL
Acta Trop. 68 (1), 105-114 (1997)
MEDLINE
98013247
PUBMED
9352006
REFERENCE
2 (bases 1 to 594)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct Submission
JOURNAL
Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore
FEATURES
Location/Qualifiers
source
1. .594
/organism="Plasmodium vivax"
/isolate="primary isolate pv13/p"
/db_xref="taxon:5855"
/note="extrachromosomal plastid"
rRNA
<1..>594
/product="large subunit ribosomal RNA"
BASE COUNT
225 a 72 c 99 g 198 t
ORIGIN

Query Match 93.0%; Score 552.4; DB 3; Length 594;
Best Local Similarity 95.8%; Pred. No. 3.4e-67;
Matches 568; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 GTATCGCTTTAATAGGCGAAGACAGACTTACCCCTTAAACATCTACTGCTTACGATGCGA 60
Db 594 GTATCGCTTTAATAGGCGAAGACAGACTTACCCCTTAAACATCTACTGCTTACGATGCGA 535
Qy 61 TAAGCCGACATCGAGTGCAGAACCTTTTCGTCGAATATGACATCTCGGAAAAAGATTAGCC 120
Db 534 TAAGCCGACATCGAGTGCAGAACCTTTTCGTCGAATATGACATCTCGGAAAAAGATTAGCC 475
Qy 121 TGTATCCCTAGAGTAACTTTTATCGTTAAGCGATAATTTTATTATTAATAATATCG 180
Db 474 TGTATCCCTAGAGTAACTTTTATCGTTAAGCGATAATTTTATTATTAATAATATCG 415

QY 181 GATCATTAAAGACCGACATTAAATCTCTGTTTAAATTTTGTAATTTTACAGTTAAATATATAT 240
Db 414 GATCATTAAAGACCGACATTAAATCTCTGTTTAAATTTTGTAATTTTACAGTTAAATATATAT 355
QY 241 TTATCTTTTATATAATAAATAACAATTTGTACACCTCGTTTTTATATATAGGAGGAGACCGC 300
Db 354 ATATCTTTTATATAACAATATAAATTTGTACTCTCTCGTTTTTATATAGGAGGAGACCGC 295
QY 301 CCAGTCAAACTATCTTATAAATATTTGTTAAATAATTTGTTATAAATAATTTTATAAGAAT 360
Db 294 CCAGTCAAACTATCTTATAAATATTTGTTAAATAATTTGTTATAAATAATTTTATAAGAAT 235
QY 361 TTATATATATAAATAAATGTTATTTTCAATTAACAATACATTTTCCAAAAATAATATT 420
Db 234 TTATATATATAAATAAATGTTATTTTCAATTAACAATACATTTTCCAAAAATAATATC 175
QY 421 ACTACTTCCCAATTTATCTATGTTATATATATATTTTCAATTAACAATATTAATAGTAAAG 480
Db 174 ATTATTTCCCAATTTATCTATGTTATATATATATTTTCAATTAACAATATTAATAGTAAAG 115
QY 481 CTTCATAGGGCTTTCTGCTCTAATAAAGAAATCTGCATCTTCACAGATAATTTTATT 540
Db 114 CTTCATAGGGCTTTCTGCTCTAATAAAGAAATCTGCATCTTCACAGATAATTTTATT 55
QY 541 CATTAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTACATCTTTTCATGCAGGTC 594
Db 54 CATTAAGATTTTTTTTAAAGACAGCATTTAAAGTCGTTACATCTTTTCATGCAGGTC 1

RESULT 6
PMU97565/c
LOCUS
DEFINITION
Plasmodium malariae extrachromosomal plastid large subunit
ribosomal RNA gene, partial sequence.
ACCESSION
U97565
VERSION
U97565.1
KEYWORDS
GI:4100403
SOURCE
Plasmodium malariae.
ORGANISM
Plasmodium malariae
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 593)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL
Acta Trop. 68 (1), 105-114 (1997)
MEDLINE
98013247
PUBMED
9352006
REFERENCE
2 (bases 1 to 593)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct Submission
JOURNAL
Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore
FEATURES
Location/Qualifiers
source
1. .593
/organism="Plasmodium malariae"
/isolate="primary isolate pv16/1"
/db_xref="taxon:5858"
/note="extrachromosomal plastid"
rRNA
<1..>593
/product="large subunit ribosomal RNA"
BASE COUNT
227 a 70 c 98 g 198 t
ORIGIN

Query Match 92.1%; Score 546.8; DB 3; Length 593;
Best Local Similarity 96.1%; Pred. No. 2e-66;
Matches 571; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 1 GTATCGCTTTAATAGGCGAAGACAGACTTACCCCTTAAACATCTACTGCTTACGATGCGA 60
Db 593 GTATCGCTTTAATAGGCGAAGACAGACTTACCCCTTAAACATCTACTGCTTACGATGCGA 534

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121	TGTTATCCCTPAGAGTAACTTTTATCCGTTAAGCGATAATTTATTATTAAATAATTATCG	180
473	TGTTATCCCTPAGAGTAACTTTTATCCGTTAAGCGATAATTTATTATTAAATAATTATCG	414
181	GATCATTAAAGACCGACATTAANTCTCTGTTTAAATTTTGTAATTTTACACAGTTAAATTATATAT	240
413	GATCATTAAAGACCGACATTAANTCTCTGTTTAAATTTTGTAATTTTACACAGTTAAATTATATAT	354
241	TTATCTTTTATATAATAATACATTTGTACACCTCCGTTTTTTATATAGGAGGAGACCGC	300
353	ATATCTTTTATATAACATATATAACTTTGTACTCCTCCGTTTTTATATAGGAGGAGACCGC	294
301	CCAGTCAAACTATCTTATAAATATTGTTTAAAAATTTTGGTTATAAAAATTTTATAAGAAT	360
293	CCAGTCAAACTATCTTATAAATATTGTTTAAAAATTTTGGTTA-AAAAATTTTATAAGAAT	235
361	TTATATATATATAAAATGGTATTTCATTACAAATACATTTATTCACAAAAATAATATT	420
234	TTATATATATAAAATGGTATTTCATTACAAATACATTTATTCACAAAAATAATATT	175
421	ACTACTCCCATTTATTCTATGTTATATATATATTTCAAATATCTATTAAATAGTAAAG	480
174	ATTATTTCCCATTTATGCTATGCTCTATATATATATTTTCAATATCTATTTCATAGTAAAG	115
481	CTTCAATAGGTCCTTCTGTCCTTAATAATAAGAAATCTGCATCTTTACAGATAAATTTTATTT	540
114	CTTCAATAGGTCCTTCTGTCCTTAATAATAAGAAATCTGCATCTTTACAGATAAATTTTATTT	55
541	CATTAGAATTTTTTTTAAAGACGCAATTTAAGTCGTTTACATCTTTTCATGCGAGTTC	594
54	CATTAGAATTTTTTTTAAAGACGCAATTTAAGTCGTTTACATCTTTTCATGCGAGTTC	1

```

RESULT 7
PFLSRNN/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
RNA
BASE COUNT

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PF15SRNN      2700 bp      DNA      linear      INV 27-SEP-1995
Plasmodium falciparum gene for a large subunit ribosomal RNA from
the inverted repeat within the 35-Kb circular DNA.
X61660
X61660.1      GI:13318
inverted repeat; ribosomal RNA; ribosomal RNA large subunit.
malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 2700)
Gardner,M.J.
Direct Submission
Submitted (22-AUG-1991) M.J. Gardner, Div of Parasitology, National
Inst for Medical Research, The Ridgeway - Mill Hill, London NW7
1AA, UK
2 (bases 1 to 2700)
Gardner,M.J., Feagin,J.E., Moore,D.J., Rangachari,K.,
Williamson,D.H. and Wilson,R.J.
Sequence and organization of large subunit rRNA genes from the
extrachromosomal 35 kb circular DNA of the malaria parasite
Plasmodium falciparum
Nucleic Acids Res. 21 (5), 1067-1071 (1993)
93219063
Location/Qualifiers
1. .2700
/organism="Plasmodium falciparum"
/strain="C10"
/db_xref="taxon:5833"
/dev_stage="Erythrocytic"
/clone="pf4, pf5, pf6a"
1. .2700
/note="subcellular localisation unknown"
/product="large subunit rRNA"
1175 a 199 c 324 g 1002 t

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ORIGIN

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Best Local Similarity	95.6%;	Pred. No. 4.8e-66;		
Matches 569;	Conservative 0;	Mismatches 25;	Indels 1;	Gaps
QY	1	GTATCGCTTTAATAGCGAACAGACTTACCCCTTTAAACATACTACTGCGCTTAGGATGCGA	60	
Db	2376	GTATCGCTTTAATAGCGAACAGACTTACCCCTTTAAACATACTACTGCGCTTAGGATGCGA	2317	
QY	61	TAAAGCGACATCGAGTGCCTAAACACCTTTTCGTCAATATGAGCTCTCGGAAAGATTAGCC	120	
Db	2316	TAAAGCGACATCGAGTGCCTAAACACCTTTTCGTCAATATGAGCTCTCGGAAAGATTAGCC	2257	
QY	121	TGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG	180	
Db	2256	TGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG	2197	
QY	181	GATCATTAAAGACCGACATTAAATCTCTGTTTAAATTTCTGAAATTTACAGTTAAATATATAT	240	
Db	2196	GATCATTAAAGACCGACATTATCTCTGTTTAAATTTCTGAAATTTACAGTTAAATATATAT	2137	
QY	241	T-TATCTTTATATATAATAATATAACATTTGTACACCTCCGTTTTTATATAGGAGGAGACCG	299	
Db	2136	TATATCTTTATATAATAATAATAACATTTGTACTCCCTCGTTTATATATATAGGAGGAGACCG	2077	
QY	300	CCCCAGTCAAACTATCTTATAATATGTTTAAAAAATTTGTTATAAAAATTTTATAGAA	359	
Db	2076	CCCCAGTCAAACTATCTATAAATATGTTTAAAAAATTTGTTATAAAAATTTTCTATAGAA	2017	
QY	360	TTTATATATATATAAAATGGTATTTTCATTAAACAATTACATATATTTCCAAAAAATAATAT	419	
Db	2016	TTTATATATAAATAAAATGGTATTTTCATTTTTAACTAAATATATTTCCAAAGAAAAATAT	1957	
QY	420	TACTACTTCCCATTTATCTCTATGTTATATATATATATATTTTCAATATCTATTAATAGTAA	479	
Db	1956	TATGTTTTCCTCATTTATAGTATGTTTAAATATATATATATTTTTCATTTTATTAATAGTAA	1897	
QY	480	GCTTCATAGGTCCTTCTCTCTCAATATATAAGAAATCTGCATCTTCACAGATAATTTTAT	539	
Db	1896	GCTTCATAGGTCCTTCTCTCTCAATATATAAGAAATCTGTATCTTCACAGATAATTTTAT	1837	
QY	540	TCATTAAAGATTTTTTTTAAAGACAGCATTTAAGTCGTTACATCTTTCATCGAGTC	594	
Db	1836	TCATTAAAGATTTTTTTTAAAGACAGCATTTAAGTCGTTACATCTTTCATCGAGTC	1782	

RESULT 8	
LOCUS	pPFRNA/c
DEFINITION	circular INV 01-AUG-1993
ACCESSION	X75545
VERSION	X75545.1 GI:520908
KEYWORDS	large ribosomal subunit; small ribosomal subunit RNA; transfer RNA-Ala; transfer RNA-Arg; transfer RNA-Asn; transfer RNA-Ile; transfer RNA-Leu; transfer RNA-Thr; transfer RNA-Val; trna gene; trnI gene; trnL gene; trnM gene; trnN gene; trnR gene; trnT gene; trnV gene.
SOURCE	malaria parasite P. falciparum.
ORGANISM	Plasmodium falciparum
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS	1 (bases 1 to 5142) Gardner,M., Preiser,P., Rangachari,K., Moore,D., Feagin,D., Williamson,D.H. and Wilson,R.J.
TITLE	Nine duplicated trna genes on the plastid-like DNA of the malaria parasite Plasmodium falciparum
JOURNAL	Gene 140, 307-308 (1994)
REFERENCE	2 (bases 1 to 5142)
AUTHORS	Wilson,R.J.M.
TITLE	Direct Submission
JOURNAL	Submitted (02-NOV-1993) R.J.M. Wilson, National Institute for Medical Research, Mill Hill, London NW7 1AA, UK
FEATURES	Location/Qualifiers

source 1. .5142
/organism="Plasmodium falciparum"
/strain="BW (C10)"
/db_xref="taxon:5833"
/chromosome="35kb circular DNA"
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/clone="HindIII (frag5)"
complement(16. .89)
/gene="trnI"
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complement(16. .89)
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complement(237. .1663)
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/gene="trnA"
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2220. .2293
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2220. .2293
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/gene="LSU rRNA"
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2335. .5030
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5045. .5117
/gene="trnT"
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BASE COUNT 2078 a 495 c 561 g 2007 t 1 others
ORIGIN

Query Match 91.4%; Score 543; DB 3; Length 5142;
Best Local Similarity 95.6%; Pred. No. 4.2e-66;
Matches 569; Conservative 0; Mismatches 25; Indels 1; Gaps 1;
QY 1 GTATCGCTTTAATAGCGAAGACAGACTTACCCCTTAAACATACACTACTGCGCTTAGGATGCGA 60
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DB 4705 GTATCGCTTTAATAGCGAAGACAGACTTACCCCTTAAACATACACTACTGCTTTAGGATGCGA 4646
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QY 61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGAAGTCTCGGAAAGATAGCC 120
Db 4645 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGAAGTCTCGGAAAGATAGCC 4586
QY 121 TGTATCCCTAGAGTAACTTTTATCCGTTAAGCGCAATTTTATTTATTAATAATTATCG 180
Db 4585 TGTATCCCTAGAGTAACTTTTATCCGTTAAGCGCAATTTTATTTACTAAATAATTATCG 4526
QY 181 GATCATTAAAGCCGACATTAATCTCTGTTTAAATTTGTTAAATTTTACAGTAAATATATAT 240
Db 4525 GATCATTAAAGCCGACATTAATCTCTGTTTAAATTTGTTAAATTTTACAGTAAATATAT 4466
QY 241 T-TATCTTTATATAATAATAATAACATTTGACACCTCCGTTTATATATAGAGGAGACCG 299
Db 4465 TATATCTTTATATAATAATAATAACATTTGACACCTCCGTTTATATATAGAGGAGACCG 4406
QY 300 CCCAGTCAAACTATCTTATAAATAATTTGTTAAATTTTGTATATAAATAATTTTATAAGAA 359
Db 4405 CCCAGTCAAACTATCTTATAAATAATTTGTTAAATTTTGTATATAAATAATTTTATAAGAA 4346
QY 360 TTTATATATATAAATAATGTTTCAATTAACAATTTACATTTTCCAAAAATAATAT 419
Db 4345 TTTATATATAAATAAATGTTTCAATTTTCACTAAATTTTCCAAAGAAATAATAT 4286
QY 420 TACTACTCCCATTTATCTATGTATATATATATATATATTTCAATATCTATTAATAGTAAA 479
Db 4285 TATTGTTCCCATTTATCTATGTATATAAATAATTTTCAATTTTCAATATTTTATTAAGTAAA 4226
QY 480 GCTTCATAGGCTCTTCTGTCCTAATAATAAGAAATCGCATCTTCACAGATAATTTTATT 539
Db 4225 GCTTCATAGGCTCTTCTGTCCTAATAATAAGAAATCGCATCTTCACAGATAATTTTATT 4166
QY 540 TCATTAAAGATTTTAAAGACAGCAATTTAAGTCGTTTACATCTTTTCATGCGAGTTC 594
Db 4165 TCATTAAAGATTTTAAAGACAGCAATTTAAGTCGTTTACATCTTTTCATGCGAGTTC 4111

RESULT 9
PFCONS/PIRA 15421 bp DNA linear INV 14-FEB-1997
LOCUS P. falciparum complete gene map of plastid-like DNA (IR-A).
DEFINITION X95275
ACCESSION X95275
VERSION X95275.1 GI:1171583
KEYWORDS LSU rRNA gene; ORF 101; ORF470; ORF51; rpoB gene; rpoC gene; rpoD gene; rps2 gene; SSU rRNA gene; trnA-Ala; trnA-Arg; trnA-Asn; trnA-Ile; trnA-Leu; trnA-Met; trnA-Val.
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
REFERENCE 1 (bases 1 to 15421)
AUTHORS Wilton, R.J.M., Denny, P.W., Preiser, P.R., Rangachari, K., Roberts, K., Roy, A., Whyte, A., Strath, M., Moore, D.J., Moore, P.W. and Williamson, D.H.
TITLE Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium falciparum
J. Mol. Biol. 261 (2), 155-172 (1996)
MEDLINE 96346169
REFERENCE 2 (bases 1 to 15421)
AUTHORS Wilton, R.J.M.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-1996) R.J.M. Wilton, National Institute for Medical Research, Mill Hill, London NW7 1AA, UK
COMMENT Related sequences X52177, X57167, X61660, X74308, X75544, and X75545.
FEATURES
source 1. .15421
/organism="Plasmodium falciparum"
/strain="C10"
/db_xref="taxon:5833"
/dev_stage="erythrocytic"
/note="IR-A half of 35kb circle, putative Plastid DNA"
complement(17. .74)
/gene="trnA-Ile"
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IHNKLYNYLYYHYHFKYNYNGIILNKNKNNKYNVIFLNFYNSYYK
IYNNYFNINSVYPKKMFILKNFNIOILNKLKVNNIYFYVEKLFYLNIN
NIIKKYLFYKYTKLEFIKKYANFLLYELFKYNYKYLLNKNKYNLIYNNYI
KYUKYNINILFFKNFYNNNFHIIYKNNYIYNNNNLIYKNLILNINNL
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Query Match 91.4%; Score 543; DB 3; Length 15421;
Best Local Similarity 95.6%; Pred. No. 3.3e-66;
Matches 569; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy 1 GTATCGCTTTAATAGGCGAAGACAGACTTACCCCTTAAACATACACTACTGCTTAGGATCGGA 60
Db 4704 GTATCGCTTTAATAGGCGAAGACAGACTTACCCCTTAAACATACACTACTGCTTAGGATCGGA 4645
Qy 61 TAAGCCGACATCGAGGTCGCAACCTTTTCGTCGAATGAGCTCTCGGAAAGATTAGCC 120
Db 4644 TAAGCCGACATCGAGGTCGCAACCTTTTCGTCGAATGAGCTCTCGGAAAGATTAGCC 4585
Qy 121 TGTATCCCTAGAGTAACTTTTATCGTTAAGCGATAATTTTATTAATAAATATATCG 180
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Qy 181 GATCATTAAAGACCGACATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATATATAT 240
Db 4524 GATCATTAAAGACCGACATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATATATAT 4465
Qy 241 T-TATCTTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 299
Db 4464 TATATCTTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4405
Qy 300 CCCAGTCAAACTATCTTATAAATATGTTTAAATAATTTGTTTAAATAATTTTATAAGAA 359
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Qy 360 TTTATATATATAATAAATGTTTATTCATTAAACAAATTAATTTTCCAAAAAATAATAT 419
Db 4344 TTTATATATAATAAATAATGTTTATTCATTAACTAAATAATTTTCCAAAAAATAATAT 4285
Qy 420 TACTACTTCCCATTTATCTGTTATATATATATATATATATATATATATATATATATAT 479
Db 4284 TATGTTTCCCATTTATCTGTTATATATATATATATATATATATATATATATATATAT 4225
Qy 480 GCTTCATAGGCTCTTCTGTCCTAAATAAAGAAATCTGCAATCTTCACAGATAATTTATT 539
Db 4224 GCTTCATAGGCTCTTCTGTCCTAAATAAAGAAATCTGCAATCTTCACAGATAATTTATT 4165
Qy 540 TCATTAAAGATTTTTTTTAAAGACGACGATTTAAAGTCGGTTACATCTTTTCATCGAGGTC 594
Db 4164 TCATTAAAGATTTTTTTTAAAGACGACGATTTAAAGTCGGTTACATCTTTTCATCGAGGTC 4110

RESULT 10
PFU97560/c
LOCUS PFU97560 595 bp DNA linear INV 15-MAR-2001
DEFINITION Plasmodium falciparum extrachromosomal plasmid large subunit
ACCESSION U97560
VERSION U97560.1 GI:4100398

KEYWORDS malaria parasite P. falciparum.
SOURCE Plasmodium falciparum
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 595)
AUTHORS Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL Acta Trop. 68 (1), 105-114 (1997)
MEDLINE 98013247
PubMed 9352006
REFERENCE 2 (bases 1 to 595)
AUTHORS Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore
FEATURES
source Location/Qualifiers
1..595
/organism="Plasmodium falciparum"
/isolate="primary isolate pf18/s"
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/note="extrachromosomal plasmid"
<1..>595
/product="large subunit ribosomal RNA"
BASE COUNT 231 a 71 c 91 g 202 t
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Query Match 91.1%; Score 541.4; DB 3; Length 595;
Best Local Similarity 95.5%; Pred. No. 1.1e-65;
Matches 568; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
Qy 1 GTATCGCTTTAATAGGCGAAGACAGACTTACCCCTTAAACATACACTACTGCTTAGGATCGGA 60
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Qy 61 TAAGCCGACATCGAGGTCGCAACCTTTTCGTCGAATGAGCTCTCGGAAAGATTAGCC 120
Db 535 TAAGCCGACATCGAGGTCGCAACCTTTTCGTCGAATGAGCTCTCGGAAAGATTAGCC 476
Qy 121 TGTATCCCTAGAGTAACTTTTATCGTTAAGCGATAATTTTATTAATAAATATATCG 180
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Db 355 TATATCTTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 296
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Qy 420 TACTACTTCCCATTTATCTGTTATATATATATATATATATATATATATATATATATAT 479
Db 175 TATGTTTCCCATTTATCTGTTATATATATATATATATATATATATATATATATATAT 116
Qy 480 GCTTCATAGGCTCTTCTGTCCTAAATAAAGAAATCTGCAATCTTCACAGATAATTTATT 539
Db 115 GCTTCATAGGCTCTTCTGTCCTAAATAAAGAAATCTGCAATCTTCACAGATAATTTATT 56
Qy 540 TCATTAAAGATTTTTTTTAAAGACGACGATTTAAAGTCGGTTACATCTTTTCATCGAGGTC 594
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RESULT 11
PFU97558/c
LOCUS
DEFINITION
Plasmodium falciparum extrachromosomal plasmid large subunit
ribosomal RNA gene, partial sequence.
ACCESSION
U97558
VERSION
U97558.1 GI:4100396
KEYWORDS
malaria parasite P. falciparum.
SOURCE
Plasmodium falciparum
ORGANISM
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 595)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL
Acta Trop. 68 (1), 105-114 (1997)
MEDLINE
98013247
PubMed
9352006
REFERENCE
2 (bases 1 to 595)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct Submission
JOURNAL
Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore
LOCATION/Qualifiers
1. .595
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/isolate="primary isolate pf19/1"
/db_xref="taxon:5833"
/note="extrachromosomal plasmid"
<1. >595
/product="large subunit ribosomal RNA"
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Best Local Similarity 95.3%; Pred. No. 1.8e-65;
Matches 567; Conservative 0; Mismatches 27; Indels 1; Gaps 1;
* QY 1 GATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACACTACTGCTTAGGATCGGA 60
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Db 595 GATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACACTACTGCTTAGGATCGGA 536
QY 61 TAAGCGACATCGAGTGCGCAACACCTTTTCGTCATATGACACTCTCGGAAAGATTAGCC 120
Db 535 TAAGCGACATCGAGTGCGCAACACCTTTTCGTCATATGACACTCTCGGAAAGATTAGCC 476
QY 121 TGTATCCCTAGAGTAACCTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 180
Db 475 TGTATCCCTAGAGTAACCTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 416
QY 181 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATTATATAT 240
Db 415 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATTATATAT 356
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Db 355 TATATCTTTATATAATAATAAATAACATGTACACCTCGCTTTTATATATAGGAGGACCG 296
QY 300 CCCAGTCAAACTATCTTATAATATGTTTAAATAATTTGTTATAAAAATTTTATAAGAA 359
Db 295 CCCAGTCAAACTATCTTATAATATGTTTAAATAATTTGTTATAAAAATTTTATAAGAA 236
QY 360 TTTATATATATAATAAATGGTATTTTCATTAACAATTTACATTTATTTCCAAAAAATAATAT 419
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QY 420 TACTACTTCCCAATTTATCTATGTTATATATATATATATATTTTCAATATCTATTAAGTAA 479
Db 175 TATTGTTCCCAATTTATCTATGTTAAATATATATATATTTTTCATTTATTTATTAAGTAA 116
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Db 115 GCTTCATAGGCTCTTCTGCTCTAATAAAGAAATGCTATCTTCACAGATAATTTTATT 56
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RESULT 12
PFU97559/c
LOCUS
DEFINITION
Plasmodium falciparum extrachromosomal plasmid large subunit
ribosomal RNA gene, partial sequence.
ACCESSION
U97559
VERSION
U97559.1 GI:4100397
KEYWORDS
malaria parasite P. falciparum.
SOURCE
Plasmodium falciparum
ORGANISM
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 594)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL
Acta Trop. 68 (1), 105-114 (1997)
MEDLINE
98013247
PubMed
9352006
REFERENCE
2 (bases 1 to 594)
AUTHORS
Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE
Direct Submission
JOURNAL
Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore
LOCATION/Qualifiers
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/isolate="primary isolate pf20/1"
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/note="extrachromosomal plasmid"
<1. >594
/product="large subunit ribosomal RNA"
BASE COUNT 231 a 71 c 90 g 202 t
ORIGIN
Query Match 89.7%; Score 532.6; DB 3; Length 594;
Best Local Similarity 95.6%; Pred. No. 1.8e-64;
Matches 569; Conservative 0; Mismatches 24; Indels 2; Gaps 2;
QY 1 GATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACACTACTGCTTAGGATCGGA 60
Db 594 GATCGCTTTAATAGCGAACAGACTTACCCCTTAAACATACACTACTGCTTAGGATCGGA 535
QY 61 TAAGCGACATCGAGTGCGCAACACCTTTTCGTCATATGACACTCTCGGAAAGATTAGCC 120
Db 534 TAAGCGACATCGAGTGCGCAACACCTTTTCGTCATATGACACTCTCGGAAAGATTAGCC 475
QY 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 180
Db 474 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTATTAATAATTATCG 415
QY 181 GATCATTAAGACCGACGATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATTATATAT 240
Db 414 GATCATTAAGACCGACGATTAATCTCTGTTTAATTTGTAATTTTACAGTTAATTATATAT 355
QY 241 T-TATCTTTATATAATAATAAATAACATGTACACCTCGCTTTTATATAGGAGGACCG 299
Db 354 TATATCTTTATATAATAATAAATAACATGTACACCTCGCTTTTATATAGGAGGACCG 295
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Db 294 CCCAGTCAAACTATCTTATAAATATGTTTAAATAATTTTGTATAAAAATTTTATAAGAA 235
QY 360 TTTATATATATAATAAATGGTATTTTCATTAACAATTTACATTTATTTCCAAAAAATAATAT 419
Db 234 TTTATATATAATAAATGGTATTTTCATTTTAACTAAATTTTCCAAAGAAATAATATAT 176
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Db 416 GGATCATTAAGACCGCAATTAATCTCGTTTAATTTTGAATTTTACAGTAAATATATA 357
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Db 356 TTATATCTTTTATAATAATAATAATPAACATGTACTCTCCGTTTATATATAGGAGGACG 297
QY 299 GCCCAGTCAACTATCTTATAAATATTTGTTAAATAATTTGTTATAAAAATTTTATAAGA 358
Db 296 GCCCAGTCAACTATCTTATAAATATTTGTTAAATAATTTGTTATAAAAATTTCTATAAGA 237
QY 359 ATTATATATATAATAAATGGTATTTTCATTAAACAATTTACATTTTCCRAAAAAATAATA 418
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RESULT 15
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LOCUS Plasmodium falciparum extrachromosomal plasmid large subunit
DEFINITION ribosomal RNA gene, partial sequence.
ACCESSION U97557
VERSION U97557.1 GI:4100395
KEYWORDS malaria parasite P. falciparum.
SOURCE Plasmodium falciparum
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 595)
AUTHORS Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL Acta Trop. 68 (1), 105-114 (1997)
MEDLINE 98013247
PUBMED 9352006
REFERENCE 2 (bases 1 to 595)
AUTHORS Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore

FEATURES
source Location/Qualifiers
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/db_xref="taxon:5833"
/note="extrachromosomal plasmid"
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/product="large subunit ribosomal RNA"
BASE COUNT 229 a 77 c 93 g 196 t

Query Match 89.0%; Score 528.6; DB 3; Length 595;
Best Local Similarity 94.1%; Pred. NO. 6.2e-64;
Matches 560; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 GTATCGCTTTTAAAGCGAAGACACTTACCCTTAAACAATACTACTGCTTAGGATGCGA 60
Db 595 GTATCGCTTTTAAAGCGAAGACACTTACCCTTAAACAATACTACTGCTTAGGATGCGA 536
QY 61 TAAGCCGACATCGAGTGCCAAACCTTTTCGTCATATGAGCTCTCGGAAAGATTAGCC 120
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Db 535 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAAATATGGACTCTCGGAAAGATTAGCC 476
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